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# FIG. 1

<i>Bet v 1</i> sense	5' - AATTATGAGACTGAGACCACCTCTGTTATCCCAGCAGCTCG	-3'
<i>Bet v 1</i> non-sense	3' - TTAATACTCTGACTCTGGTGGAGACAATAGGGTCGTCGAGC	-5'
sense primer	5' - TGAGACCCCTCTGTTATCCCAG	-3'
non-sense primer	3' - ATACTCTGACTCTGGGGGAGACA	-5'

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## FIG. 2

all	sense	1: 183Bv, 15-mer 5'-GTTGCCAACGATCAG
1	sense	2: 184Bv, 23-mer 5'-TGAGACCCCTCTGTTATCCCAG
1	non-sense	3: 185Bv, 23-mer 5'-ACAGAGGGGTCTCAGTCTCATA
2	sense	4: 186Bv, 31-mer 5'-GATACCCTCTTTCCACAGGTGCACCCCAAG
2	non-sense	5: 187Bv, 31-mer 5'-ACCTGTGGAAAGAGGGTATCGCCATCAAGGA
3	sense	6: 188Bv, 23-mer 5'-AACATTTTCAGGAAATGGAGGGCC
3	non-sense	7: 189Bv, 23-mer 5'-TTTCCTGAAATGTTTTCAACACT
4	sense	8: 190Bv, 23-mer 5'-TTAAGAACATCAGCTTTCCCGAA
4	non-sense	9: 191Bv, 23-mer 5'-AGCTGATGTTCTTAATGGTTCCA
5	sense	10: 192Bv, 23-mer 5'-GGACCATGCAAACCTTCAAATACA
5	non-sense	11: 193Bv, 23-mer 5'-AGTTTGATGGTCCACCTCATCA
6	sense	12: 194Bv, 23-mer 5'-TTTCCTCAGGCCTCCCTTTCAA
6	non-sense	13: 195Bv, 23-mer 5'-AGGCCTGAGGGAAGCTGATCTT
7	sense	14: 196Bv, 24-mer 5'-TGAAGGATCTGGAGGGCCTGGAAC
7	non-sense	15: 197Bv, 24-mer 5'-CCCTCCAGATCCTTCAATGTTTTTC
8	sense	16: 198Bv, 24-mer 5'-GGCAACTGGTGTGATGGAGGATCCAT
8	non-sense	17: 199Bv, 24-mer 5'-CCATCACCAGTTGCCACTATCTTT
all	non-sense	18: 200Bv, 15-mer 5'-CATGCCATCCGTAAG

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# FIG. 3

1 (A-C)

GGTGTGTTTAATTATGAGACTGAGACCACCTCTGTTATCCCAGCAGCTCGACTGTTCAAG 60  
 G V F N Y E T E T T-P S V I P A A R L F K 20

9 (A-G) 2 (A-C) 2 (A-C)

GCCTTTATCCTTGATGGCGATAACCTCTTTCCAAAGGTTGCACCCCAAGCCATTAGCAGT 120  
 A F I L D-G G D N-T L F P K-Q V A P Q A I S S 40

3 (GA-TC) 7 (AA-TC) 4 (G-C) 6 (GA-TC)

GTTGAAAACATTGAAGGAAATGGAGGGCCTGGAACCATTAAAGAAGATCAGCTTTCCCGAA 180  
 V E N I E-S G N-S G G P G T I K K-N I S F P E-S 60

5 (CA-TG)

GGCCTCCCTTTCAAGTACGTGAAGGACAGAGTTGATGAGGTGGACCACACAACTTCAAA 240  
 G L P F K Y V K D R V D E V D H T-A N F K 80

TACAATTACAGCGTGATCGAGGGCGGTCCCATAGGCGACACATTGGAGAAGATCTCCAAC 300  
 Y N Y S V I E G G P I G D T L E K I S N 100

10 (GAG-CAC) 8 (CCC-TGG)

GAGATAAAGATAGTGGCAACCCTGATGGAGGATCCATCTTGAAGATCAGCAACAAGTAC 360  
 E I K I V A T P-G D G G S I L K I S N K Y 120

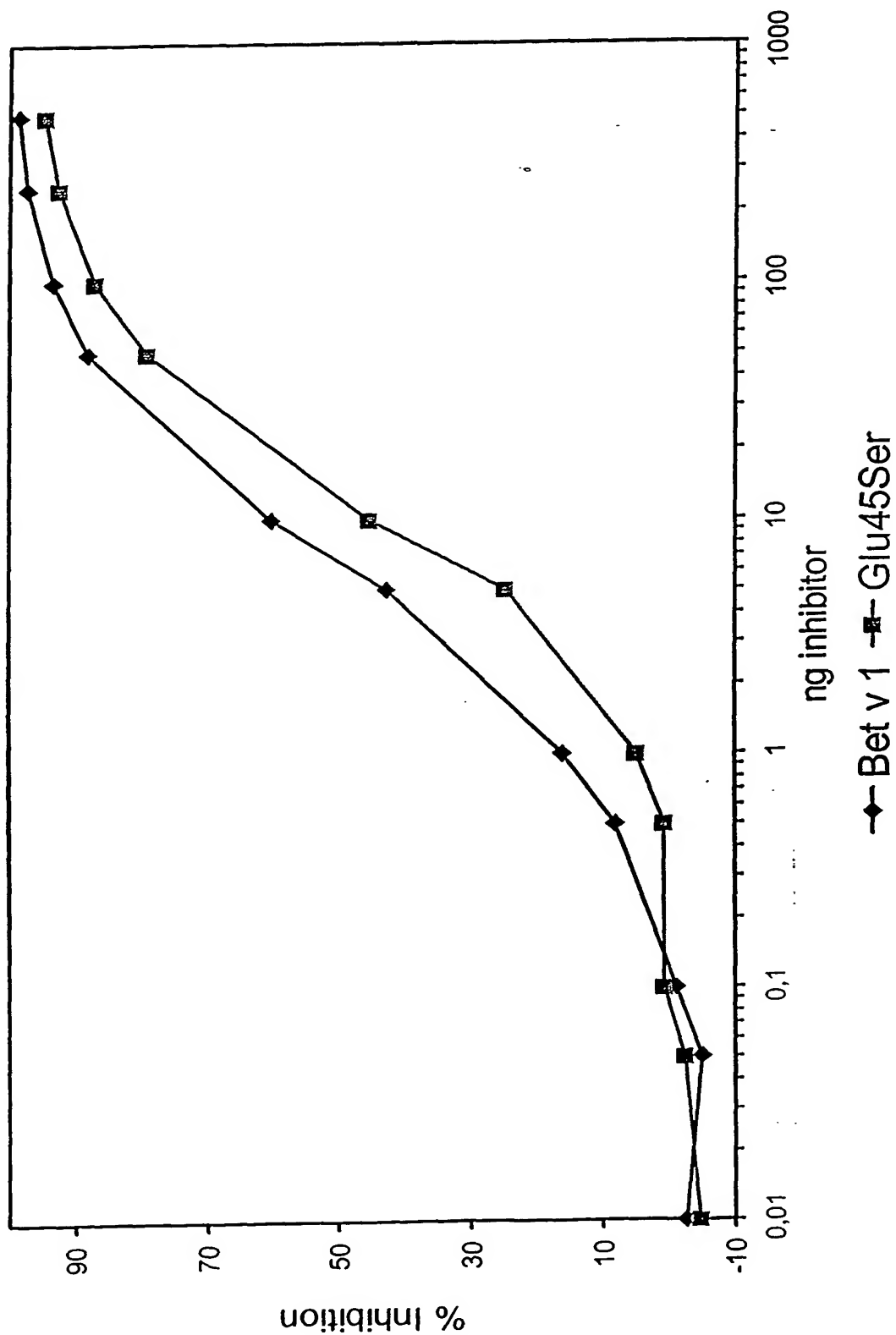
CACACCAAAGGTGACCATGAGGTGAAGGCAGAGCAGGTTAAGGCAAGTAAAGAAATGGGC 420  
 H T K G D H E V K A E Q V K A S K E M G 140

GAGACACTTTTGAGGGCCGTTGAGAGCTACCTCTTGGCACACTCCGATGCCTACAATAA 480  
 E T L L R A V E S Y L L A H S D A Y N stop 159

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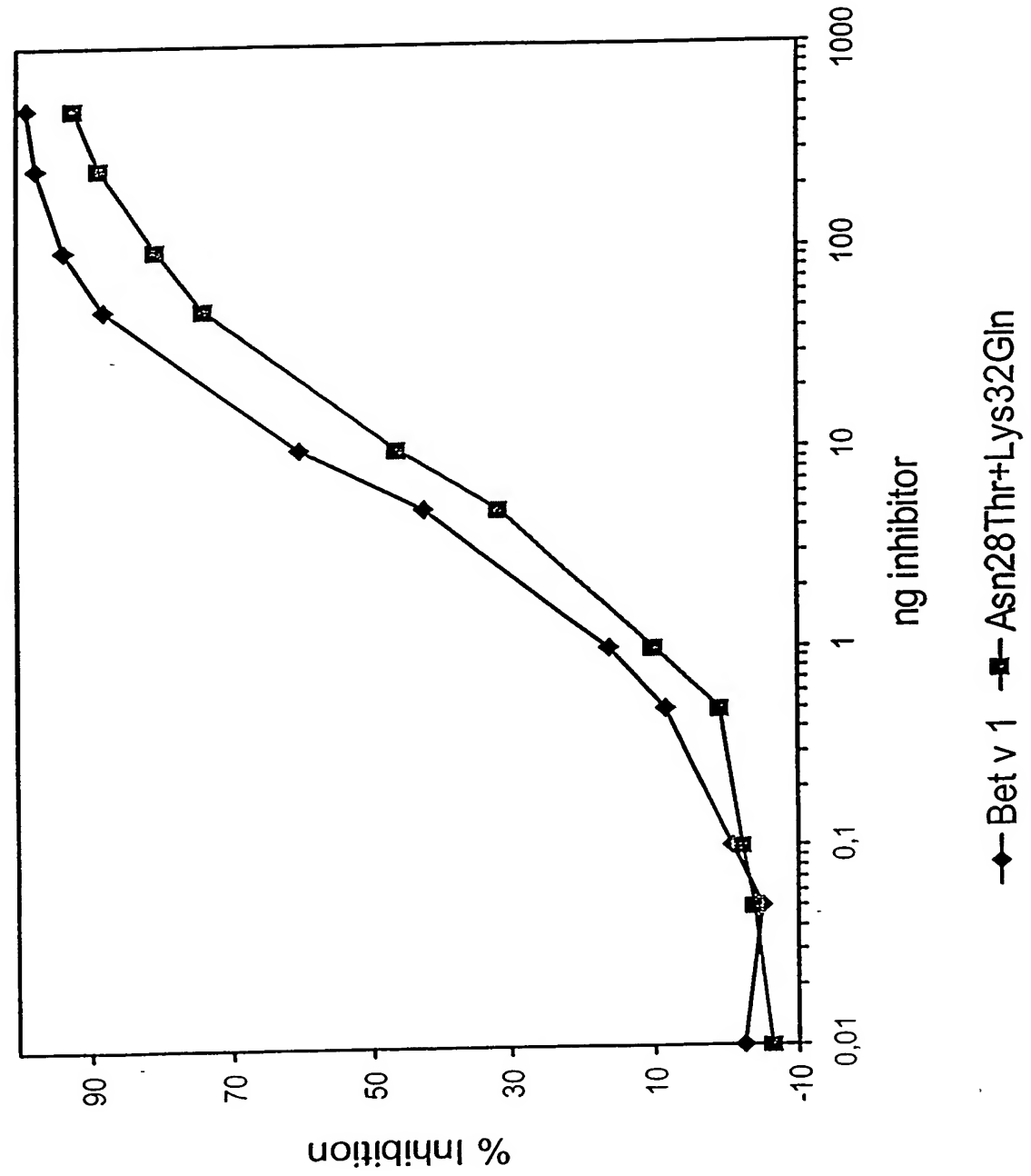
FIG. 4



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FIG. 5



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FIG. 6

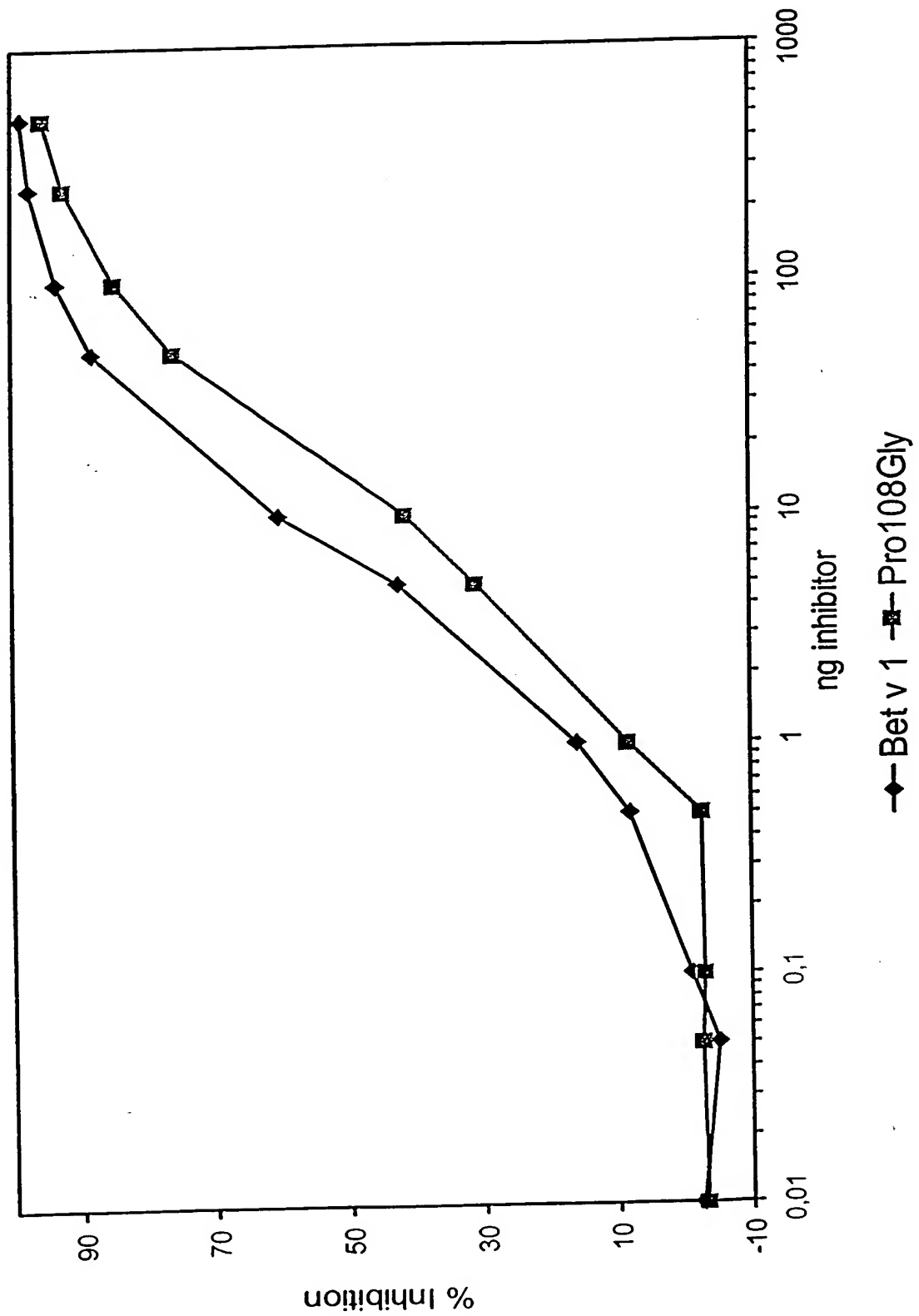
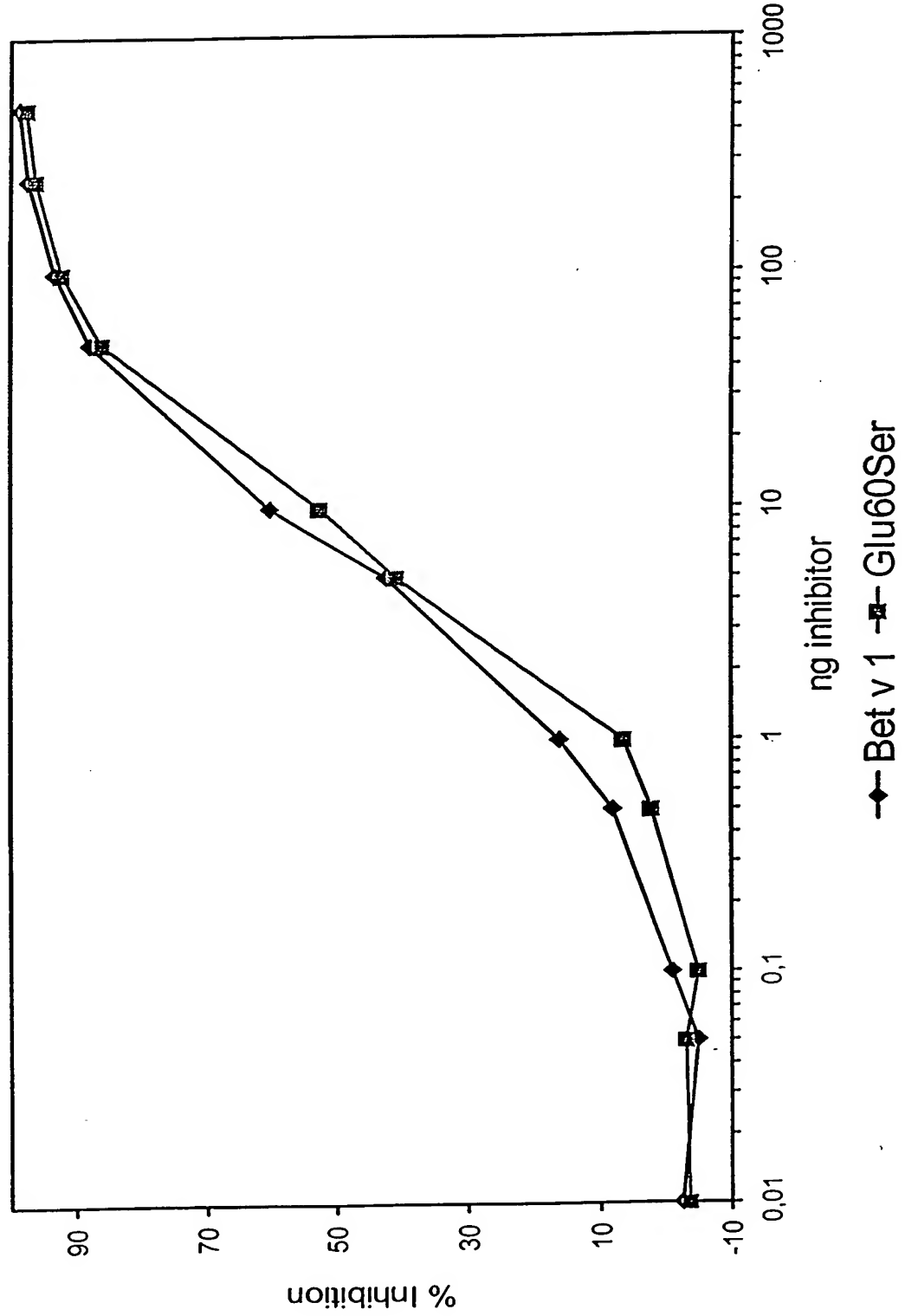




FIG. 7



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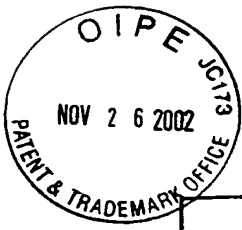
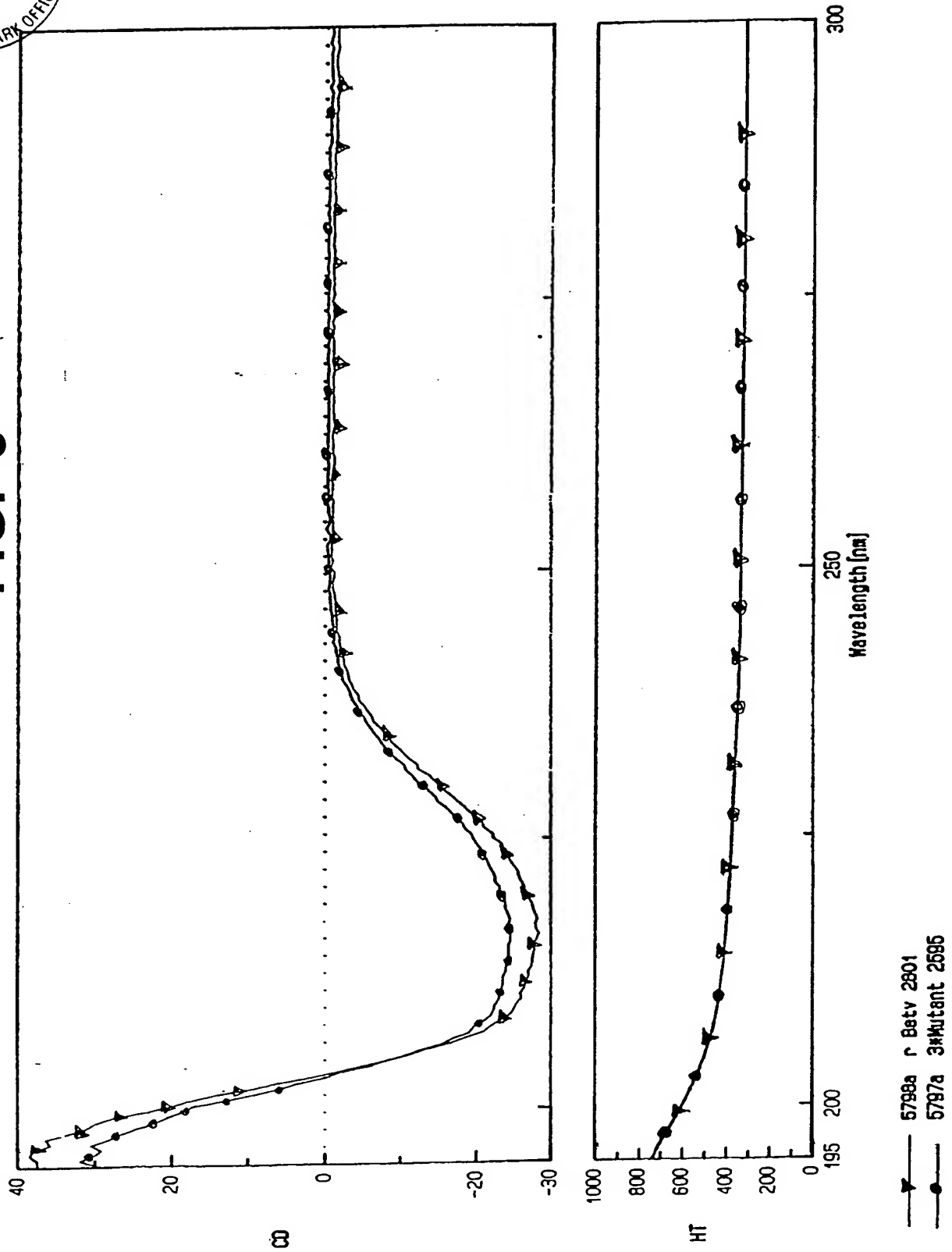


FIG. 8

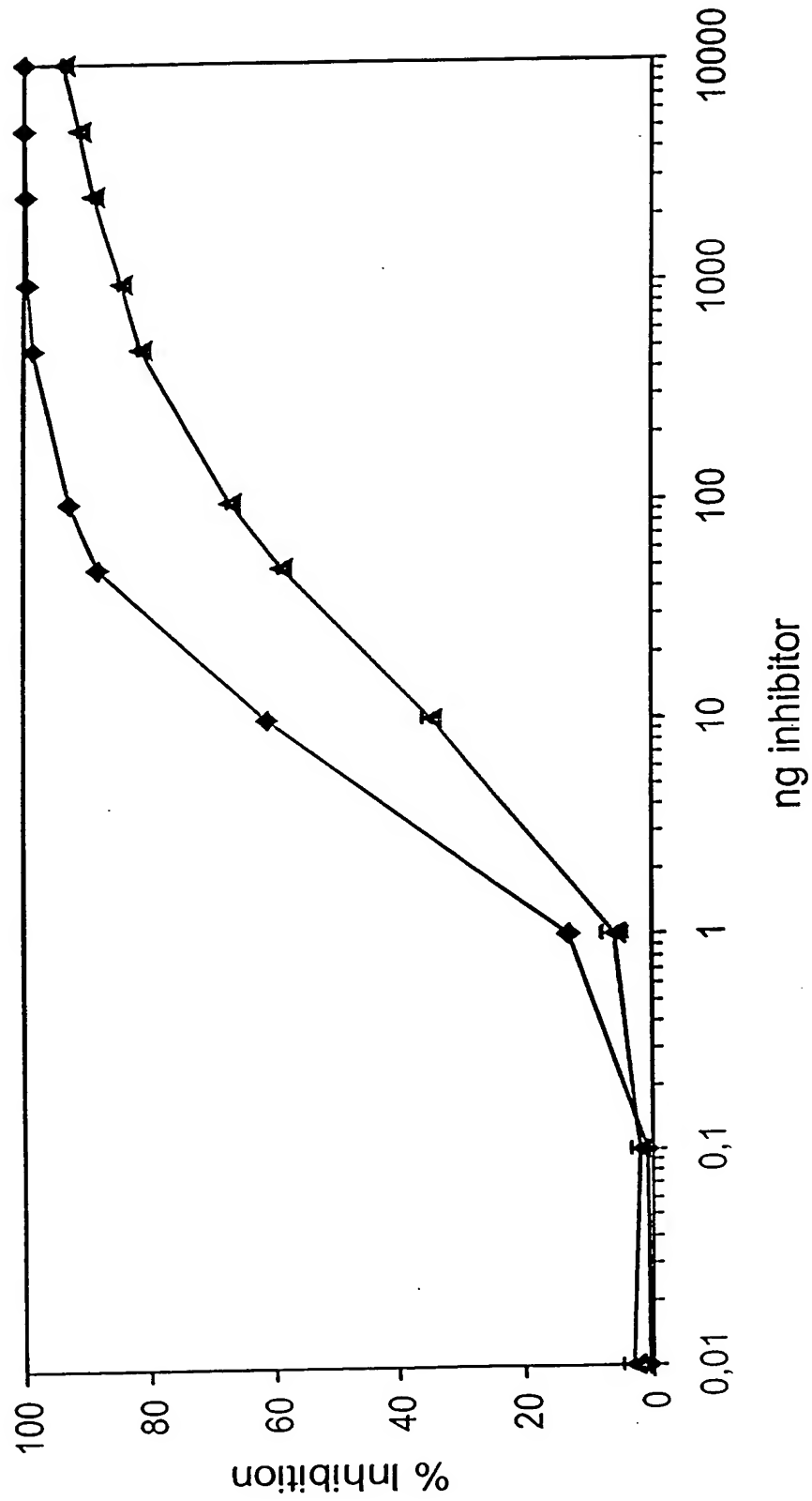




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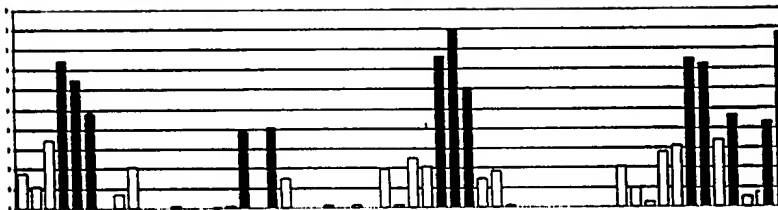
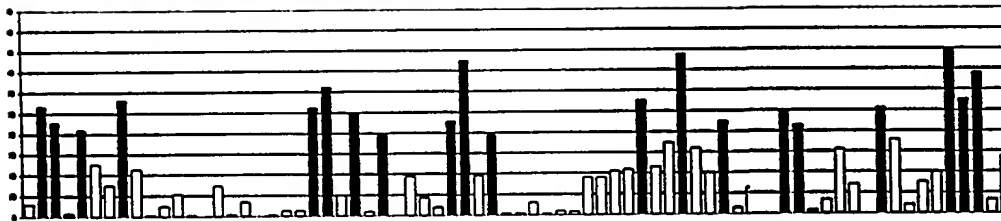
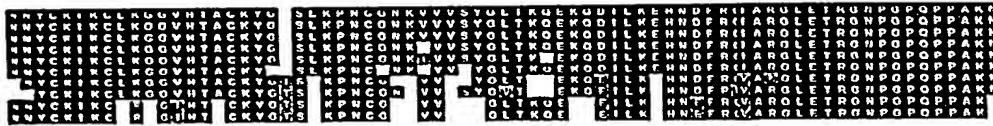
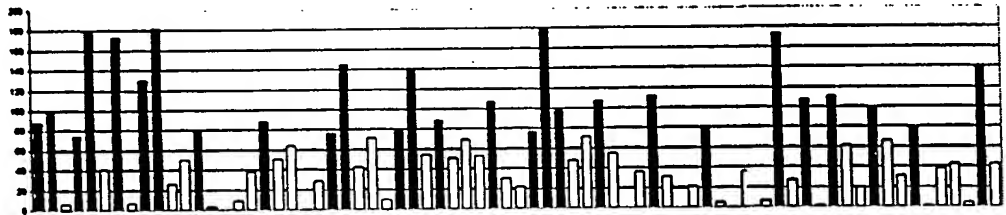


FIG. 9

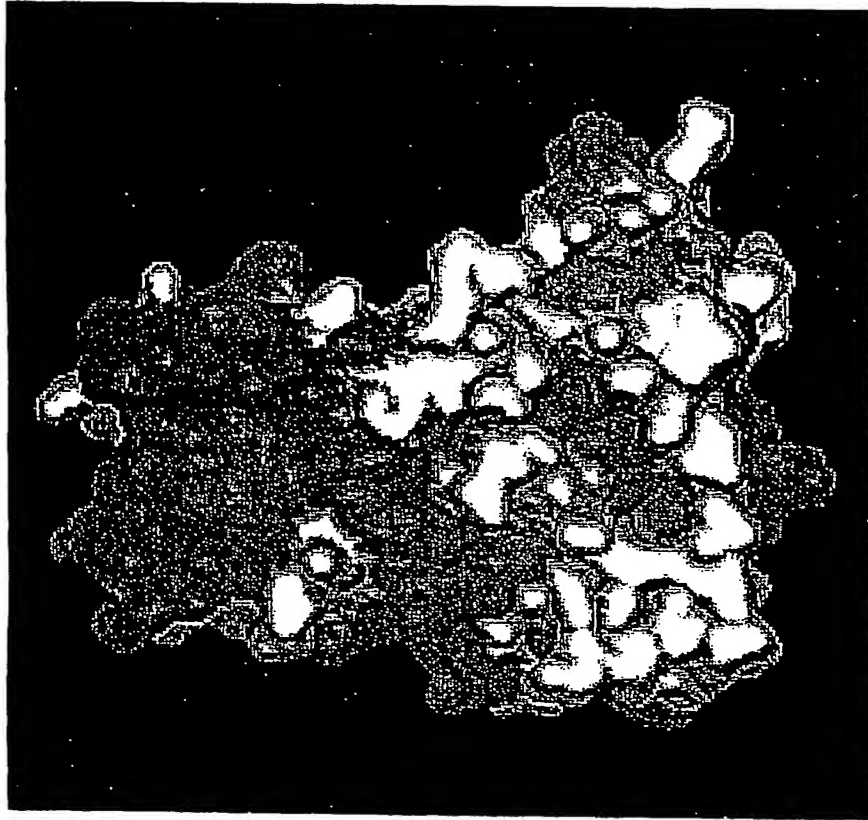


—◆— Bet v 1 —▲— Glu45Ser, Pro108Gly, Asn28Thr+Lys32Gln.

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**FIG. 10 A**

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**FIG. 10 B**

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## FIG. 11 A

Ves v 5 mutant 1 (K72A)

Ves v 5 sense	5'-	ACCACAGCCTCCAGCGAAGAATATGAAAAATTTGGTATGGA	-3'
Ves v 5 non-sense	3'-	TGGTGTCTGGAGGTCGCTTCTTATACTTTTAAACCATACCT	-5'
sense primer	5'-	CCAGCGGCTAATATGAAAAAT	-3'
non-sense primer	3'-	GTCGGAGGTCGCGATTATAC	-5'

## FIG. 11 B

Ves v 5 mutant 2 (Y96A)

Ves v 5 sense	5'-	GGCTAATCAATGTCAATATGGTCACGATACTTGCAGGGATG	-3'
Ves v 5 non-sense	3'-	CCGATTAGTTACAGTTATACCAAGTGCTATGAACGTCCTAC	-5'
sense primer	5'-	TGTCAAGCTGGTCACGATACT	-3'
non-sense primer	3'-	TTAGTTACAGTTCCGACCAAGTG	-5'

## FIG. 12

all sense 1: XhoI start, 38-mer:

EcoRI  
 5'-CCGCTCGAGAAAAGAAACAATTATTGTAAAAATAAAATG  
  L  E  K  R      N  N  Y  C  K  I  K    
 Kex2 cleavage site      amino terminus of Ves v 5

1	sense	1: K72As	21-mer	5'-CCAGCGGCTAATATGAAAAAT
1	non-sense	2: K72Aa	21-mer	5'-CATATTAGCCGCTGGAGGCTG
2	sense	3: Y96As	21-mer	5'-TGTCAAGCTGGTCACGATACT
2	non-sense	4: Y96Aa	21-mer	5'-GTGACCAGCTTGACATTGATT
all non-sense 7: CT-pPICZαA, 21-mer				5'-ATTCATCAGCTGCGAGATAGG

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## FIG. 13

1	AACAATTATTGTAAAATAAAATGTTTGAAAGGAGGTGTCCATACTGCCTGCAAATATGGA	60
1	N N Y C K I K C L K G G V H T A C K Y G	20
61	AGTCTTAAACCGAATTGCGGTAATAAGGTAGTGGTATCCTATGGTCTAACGAAACAAGAG	120
21	S L K P N C G N K V V V S Y G L T K Q E	40
121	AAACAAGACATCTTAAAGGAGCACAATGACTTTAGACAAAAAATTGCACGAGGATTGGAG	180
41	K Q D I L K E H N D F R Q K I A R G L E	60
	1 [K72A] (AAG-GCT)	
181	ACTAGAGGTAATCCTGGACCACAGCCTCCAGCGAAGAATATGAAAAATTTGGTATGGAAC	240
61	T R G N P G P Q P P A K N M K N L V W N	80
	2 [Y96A] (TA-GC)	
241	GACGAGTTAGCTTATGTGCGCCCAAGTGTGGGCTAATCAATGTCAATATGGTCACGATACT	300
81	D E L A Y V A Q V W A N Q C Q Y G H D T	100
301	TGCAGGGATGTAGCAAAATATCAGGTTGGACAAAACGTAGCCTTAACAGGTAGCACGGCT	360
101	C R D V A K Y Q V G Q N V A L T G S T A	120
361	GCTAAATACGATGATCCAGTTAAACTAGTTAAAATGTGGGAAGATGAAGTGAAAGATTAT	420
121	A K Y D D P V K L V K M W E D E V K D Y	140
421	AATCCTAAGAAAAAGTTTTTCGGGAAACGACTTTCTGAAAACCGGCCATTACACTCAAATG	480
141	N P K K K F S G N D F L K T G H Y T Q M	160
481	GTTTGGGCTAACACCAAGGAAGTTGGTTGTGGAAGTATAAAATACATTCAAGAGAAATGG	540
161	V W A N T K E V G C G S I K Y I Q E K W	180
541	CACAAACATTACCTTGTATGTAATTATGGACCCAGCGGAAACTTTAAGAATGAGGAACTT	600
181	H K H Y L V C N Y G P S G N F K N E E L	200
601	TATCAAACAAAGTAA	612
201	Y Q T K stop	204

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FIG. 14

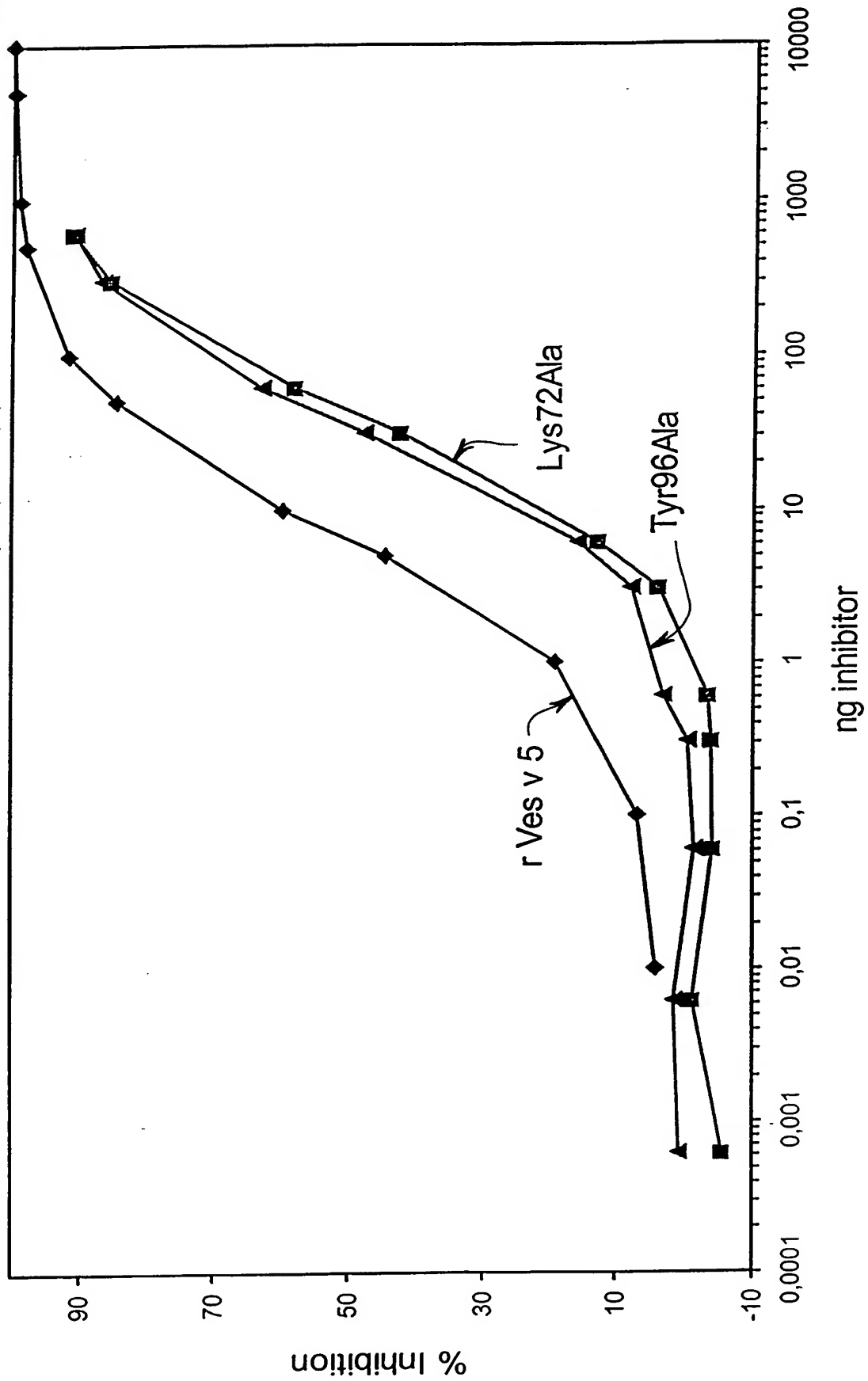
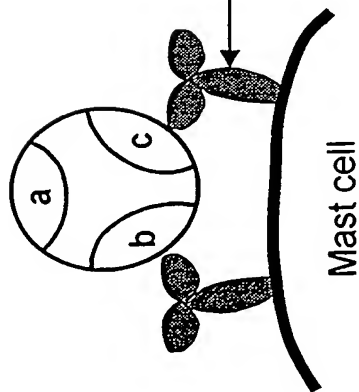
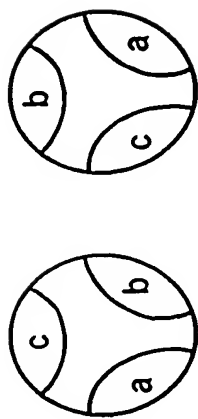


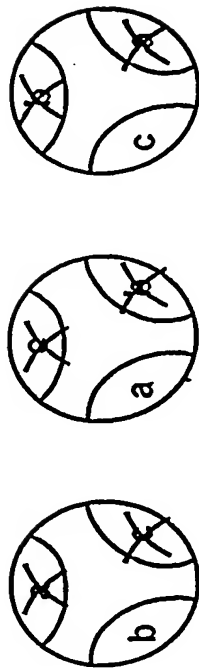


FIG. 15 A



Cross-linking

FIG. 15 B



No cross-linking

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## FIG. 16 A

### DNA SEQUENCE

#### ORIGIN

```

1      cacaaattct tctttctcc ttactactga tcattaatct gaaaacaaaa ccaaacaac
61     cattcaaaat gatgtacaaa attttgtgtc ttccattggt ggtcgcagcc gttgctcgtg
121    atcaagtcga tgtcaaagat tgtgccaatc atgaaatcaa aaaagttttg gtaccaggat
181    gccatgggtc agaaccatgt atcattcatc gtggtaaacc attccaattg gaagccggtt
241    tcgaagccaa ccaaaacaca aaaacggcta aaattgaaat caaagcctca atcgatgggt
301    tagaagtga tgttcccggt atcgatccaa atgcatgcc a ttacatgaaa tgcccattgg
361    ttaaaggaca acaatatgat attaaatata catggaatgt tccgaaaatt gcaccaaaat
421    ctgaaaatgt tgcgtcact gttaaagtta tgggtgatga tgggtgtttg gcctgtgcta
481    ttgctactca tgctaaaatc cgcgatataa tcaaacaaaa ttattgatt ttgtaatcac
541    aatgattga ttttcttcc aaaaaaaaaa taaataaaat ttgggaatt c

```

## FIG. 16 B

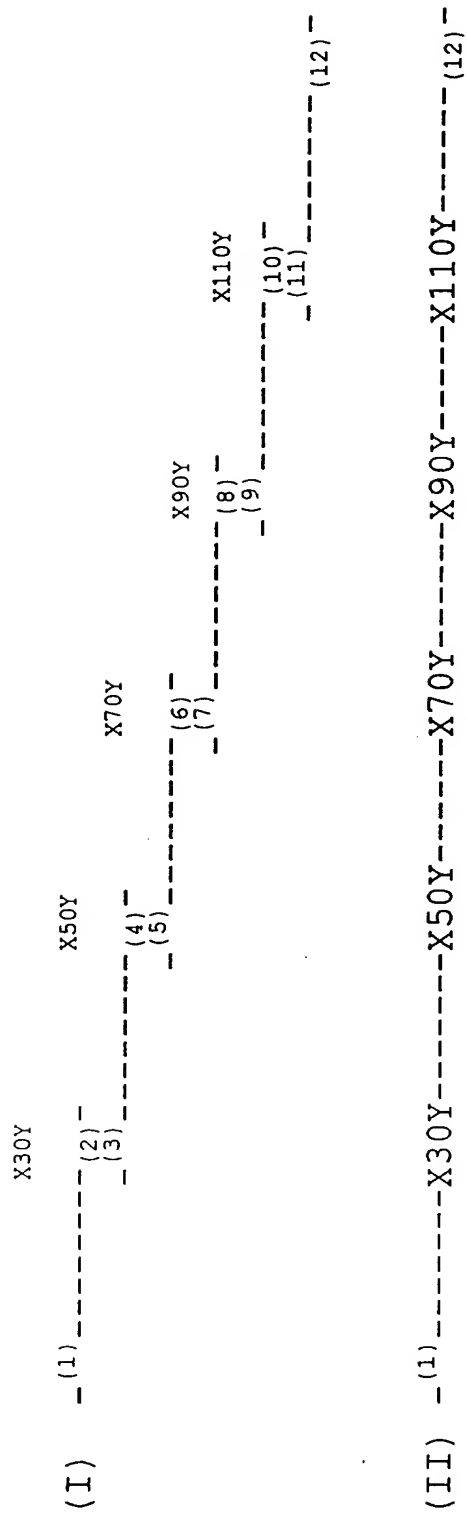
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1      mmykilclsl lvaavardqv dvkdcanhei kkvlvpgchg sepciihrk pfqleavfea
61     nqntktakie ikasidglev dvpgidpnac hymkcplvkg qqydikytwn vpkiapksen
121    vvvtkvmgd dglacaiat hakird

```



FIG. 17

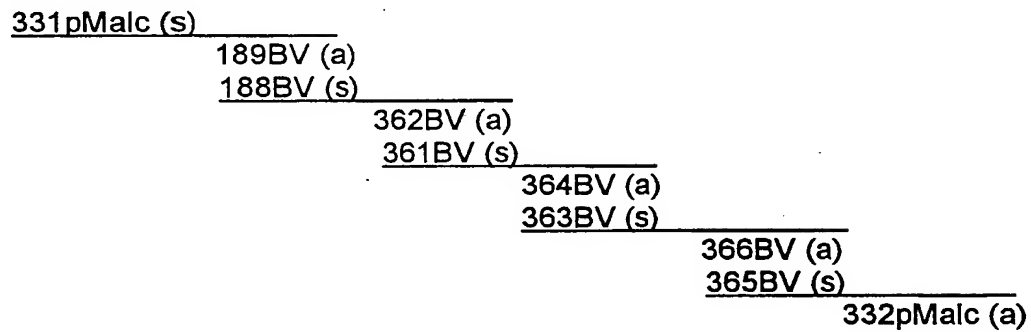


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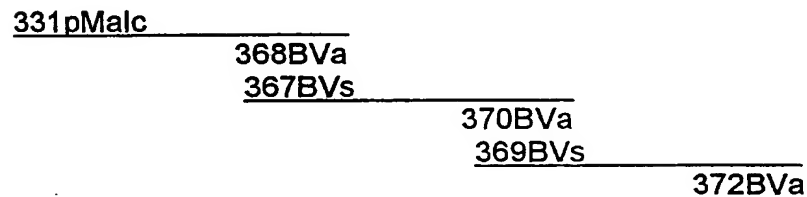
## FIG. 18 A

DNA template: Bet v 1 (2589) carrying the Y5V mutation.



## FIG. 18 B

DNA template: Bet v 1 (2571) carrying N28T, K32Q, P108G mutations.

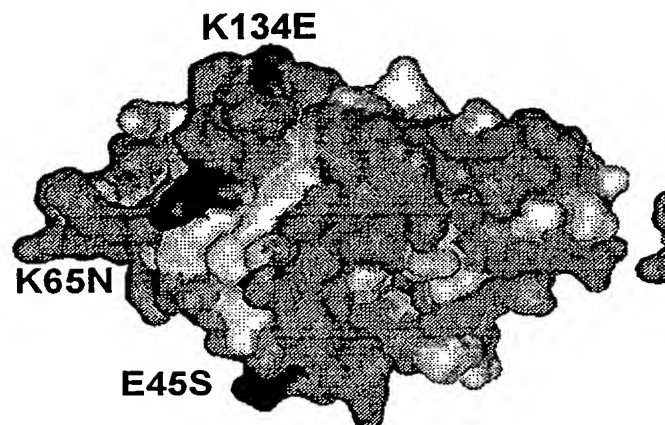
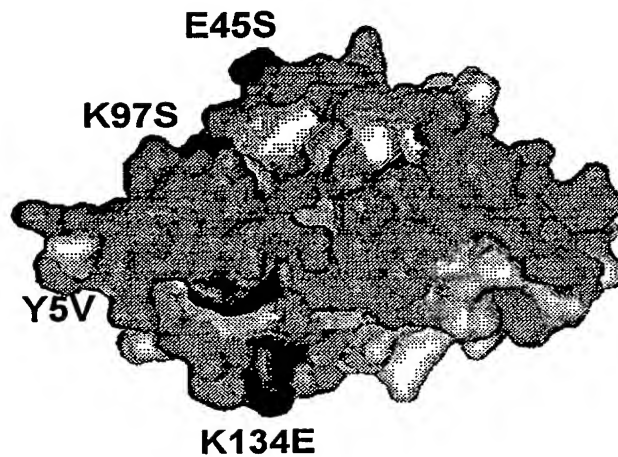
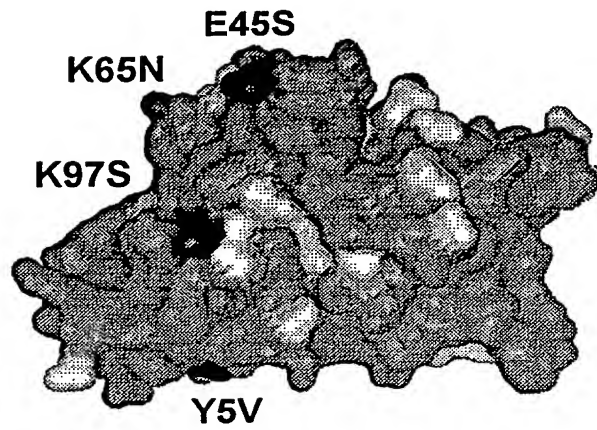


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# FIG. 19 A

Bet v 1 (2628)



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# FIG. 19 B

Bet v 1 (2637)

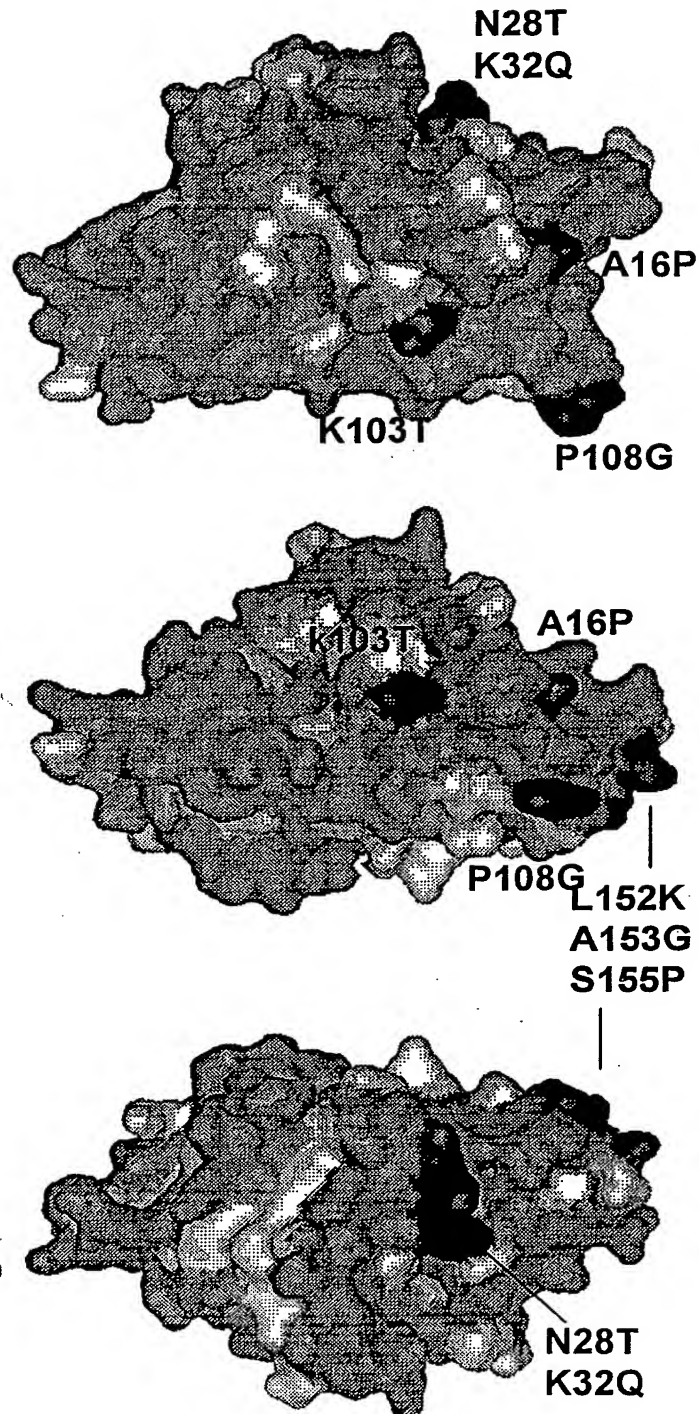




FIG. 20

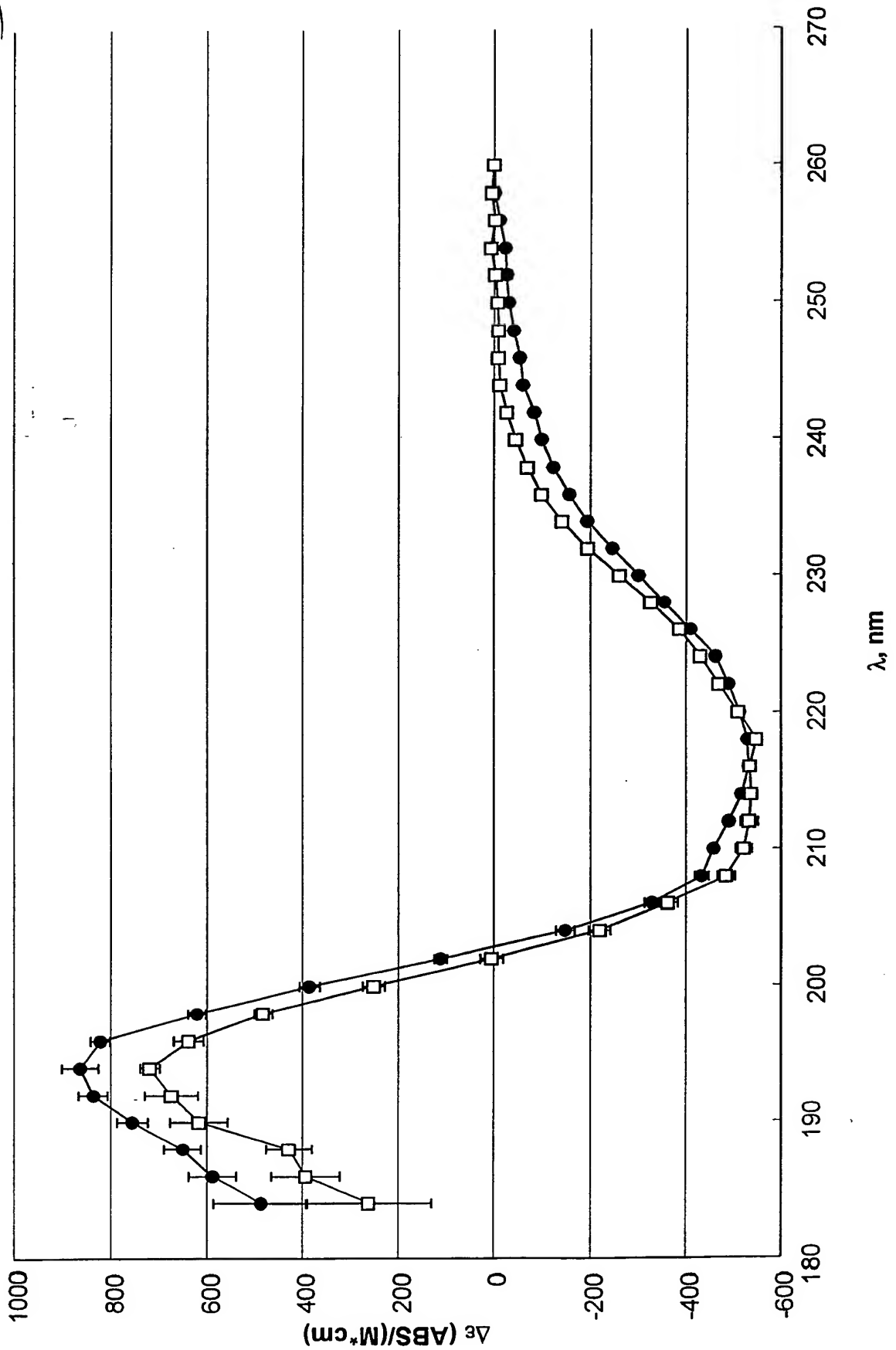
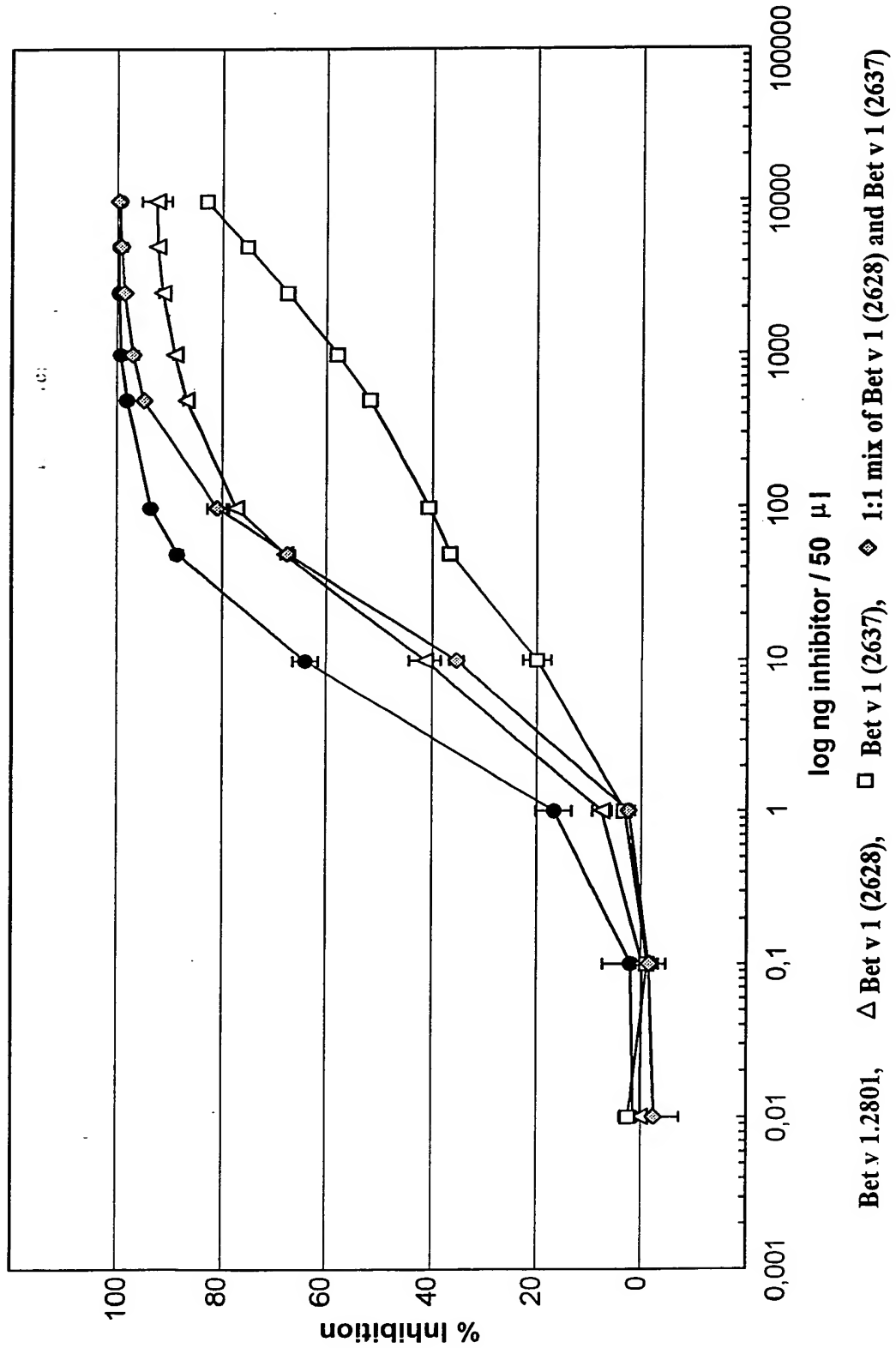




FIG. 21



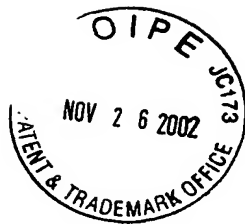


FIG. 22

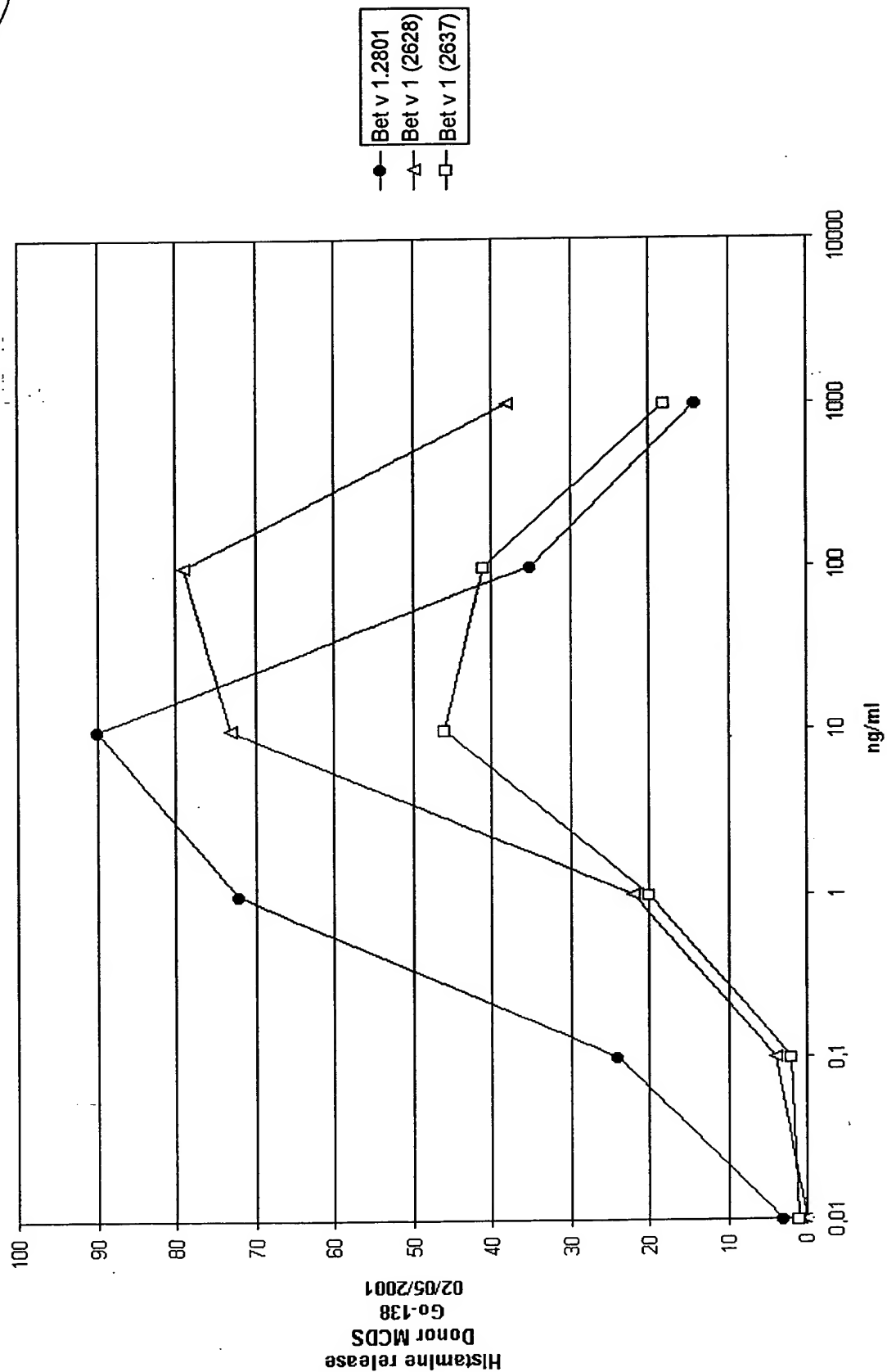


FIG. 23

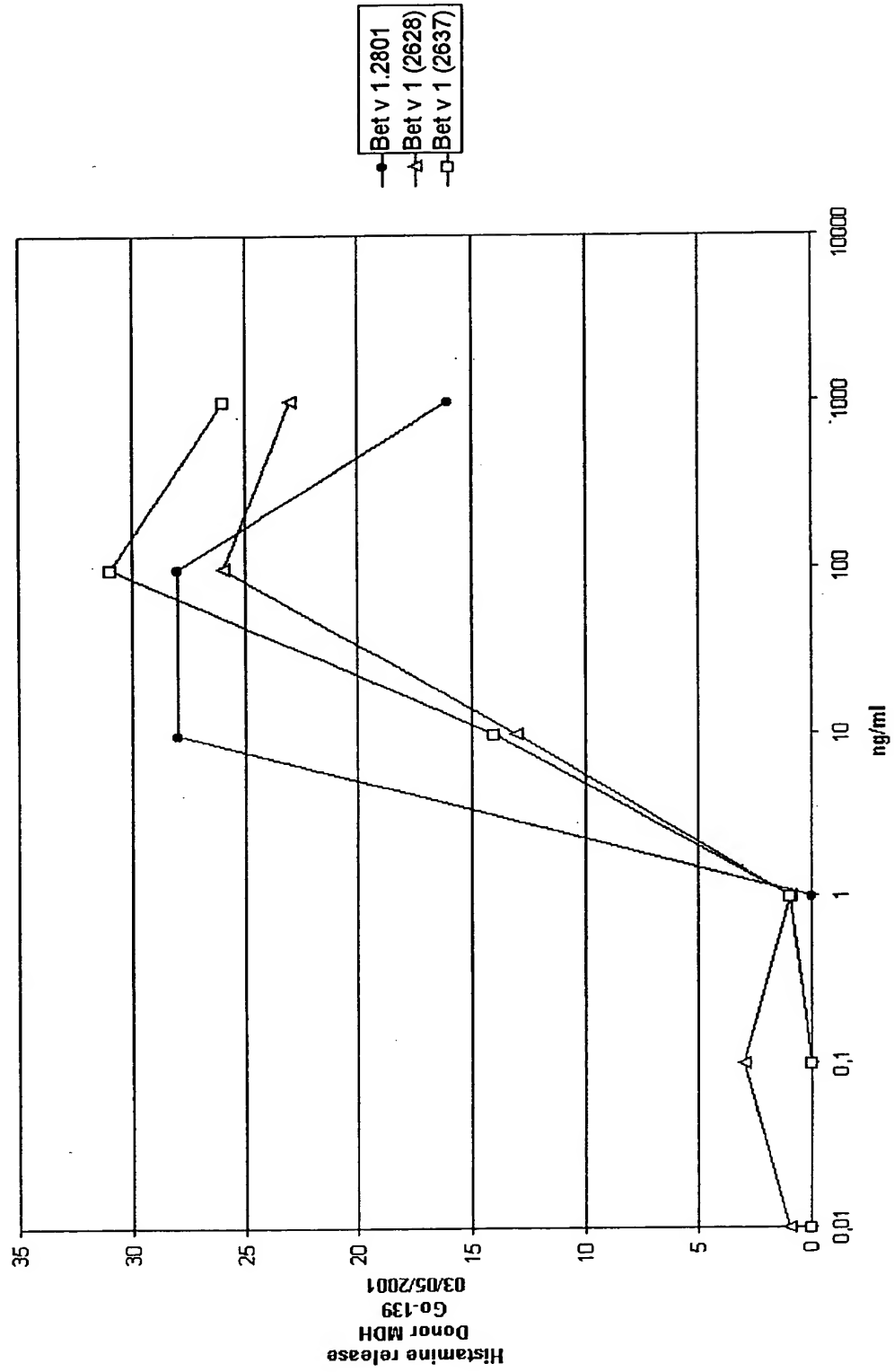
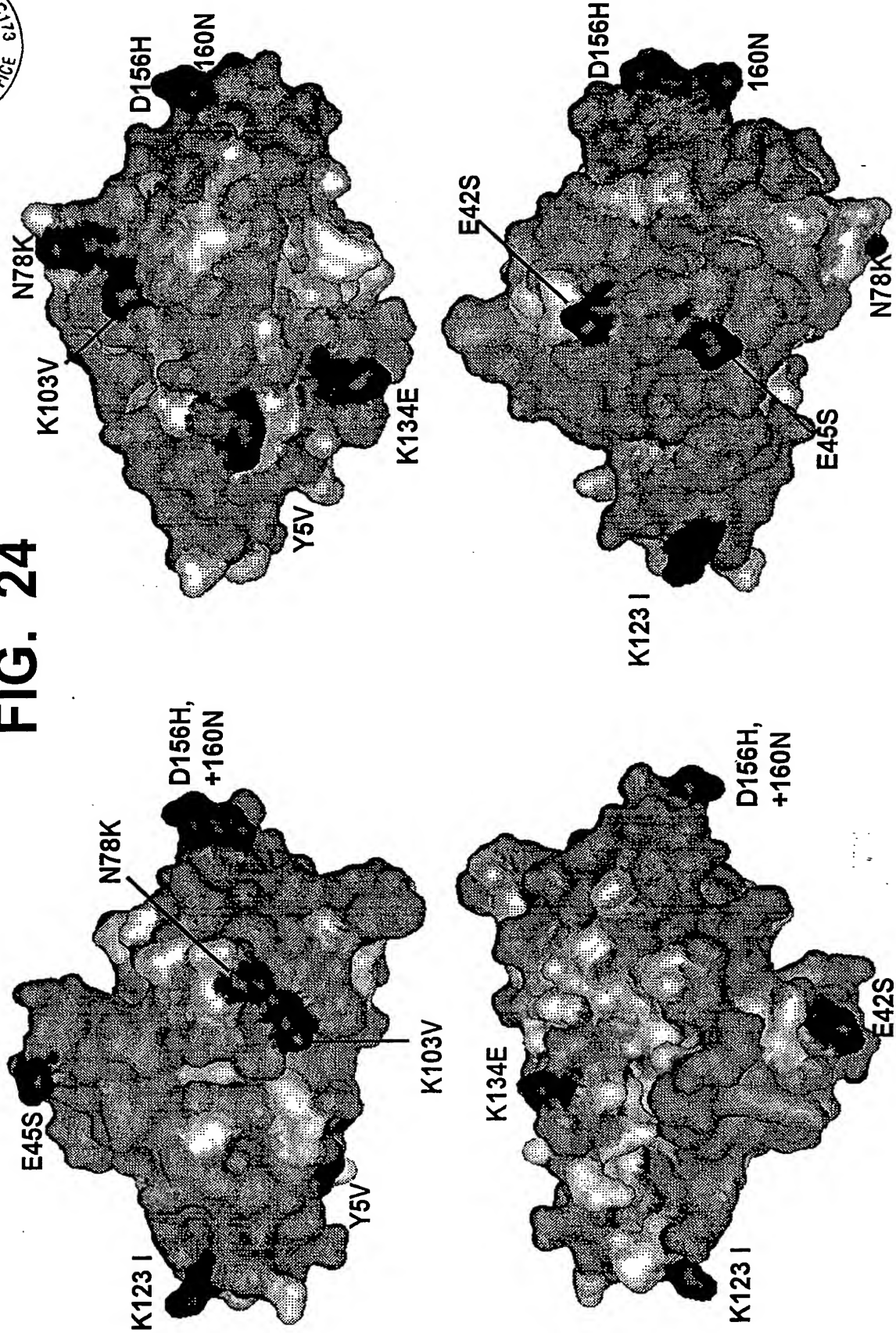




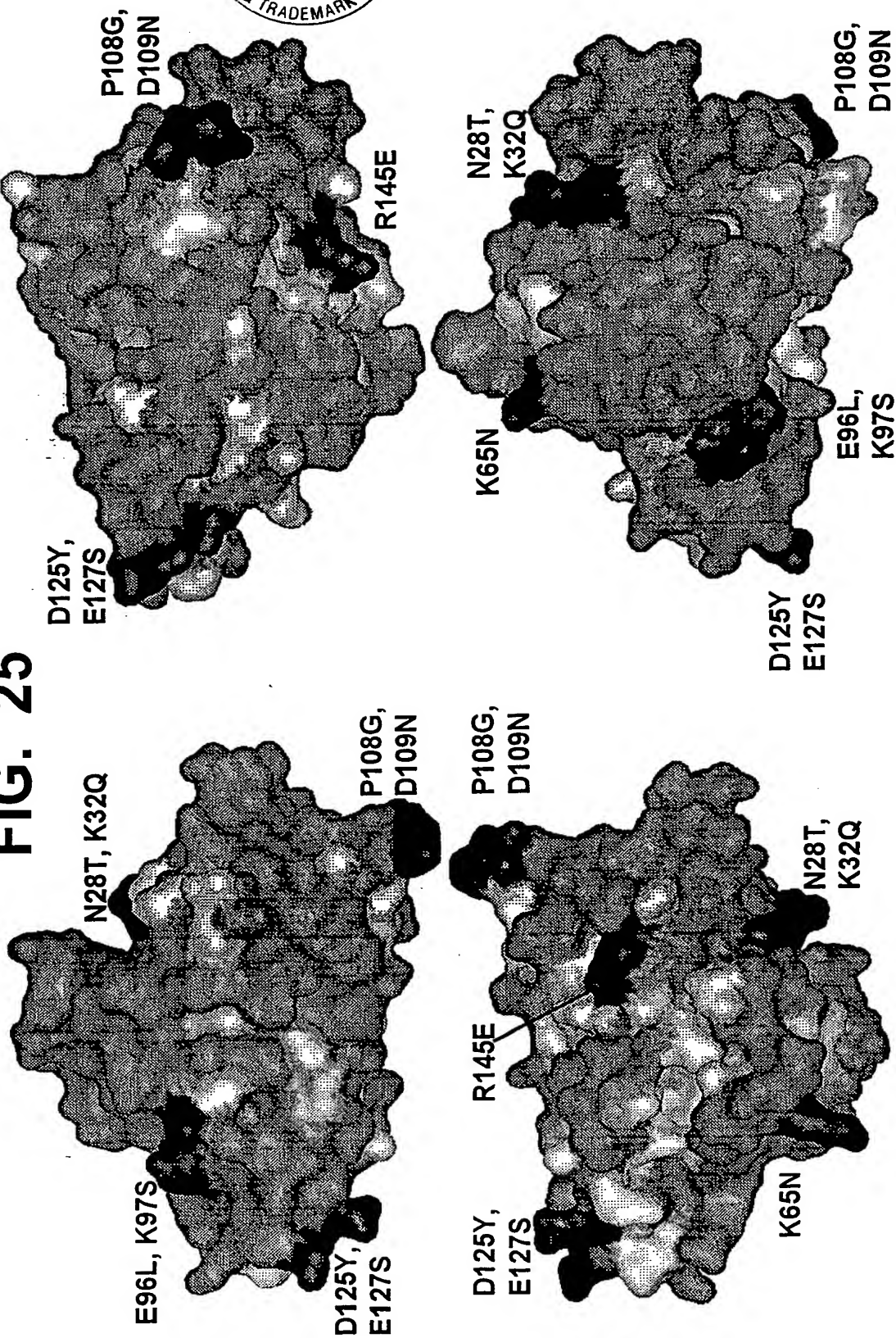
FIG. 24



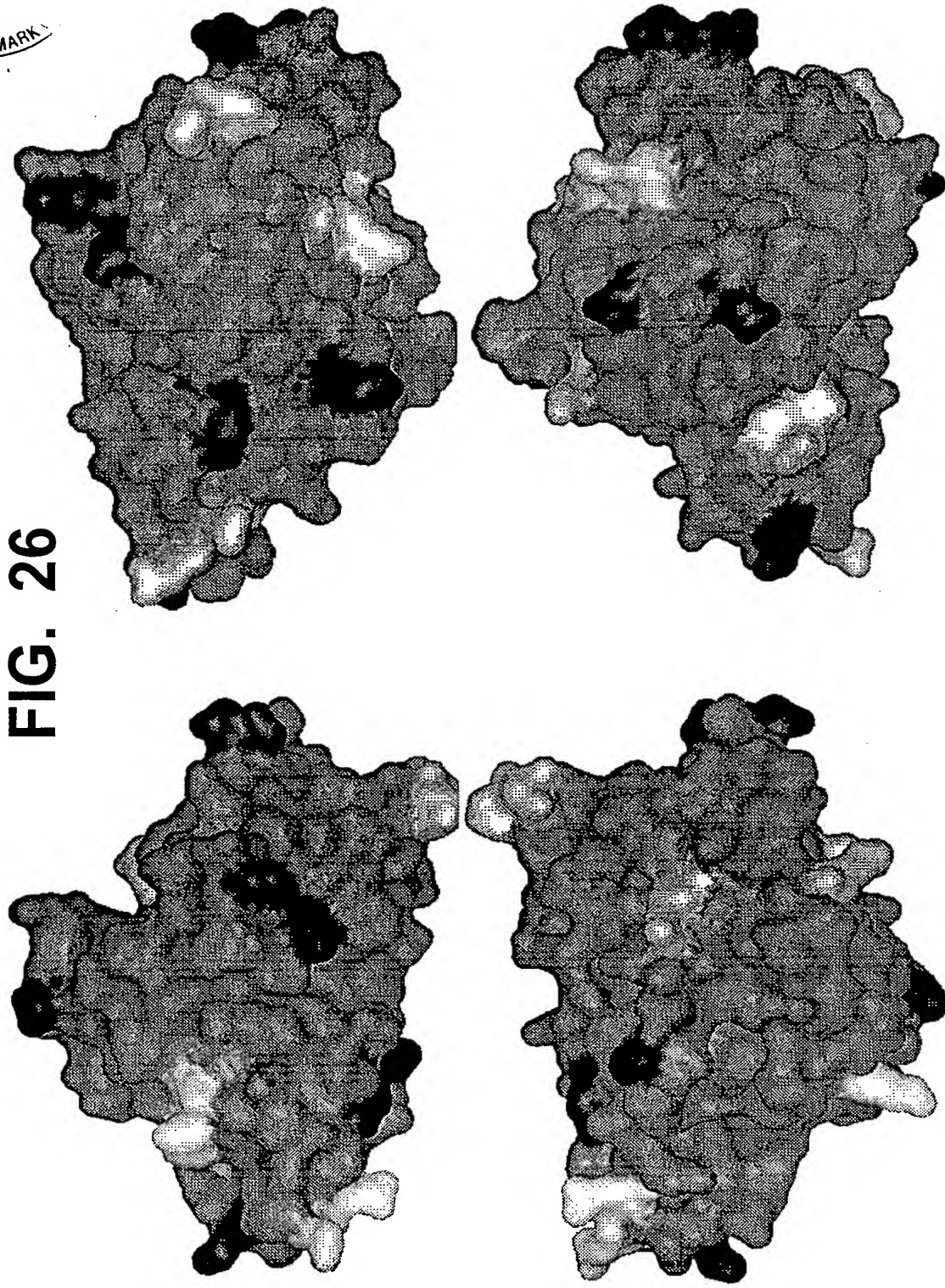
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FIG. 25



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**FIG. 26**

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FIG. 27

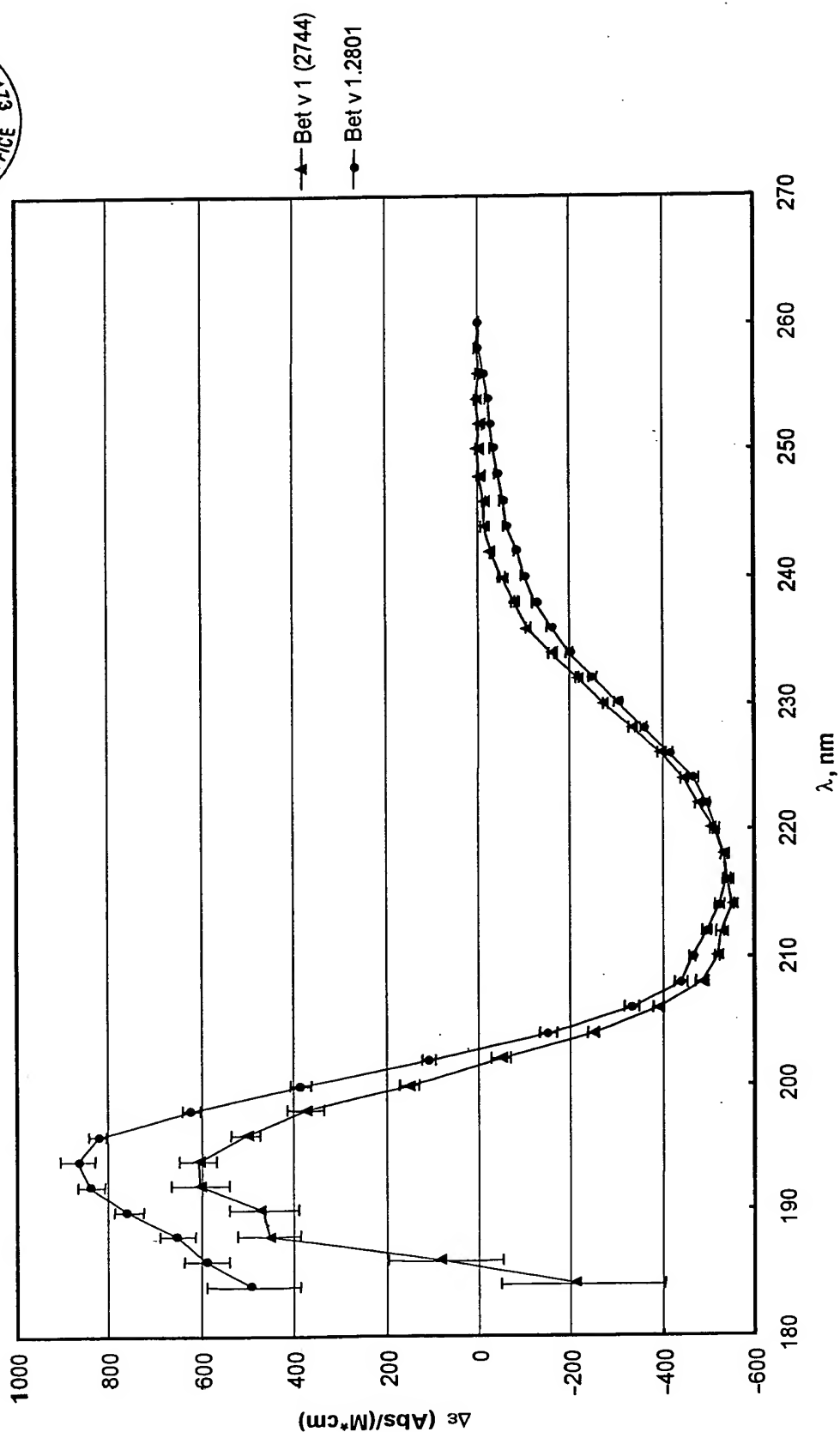
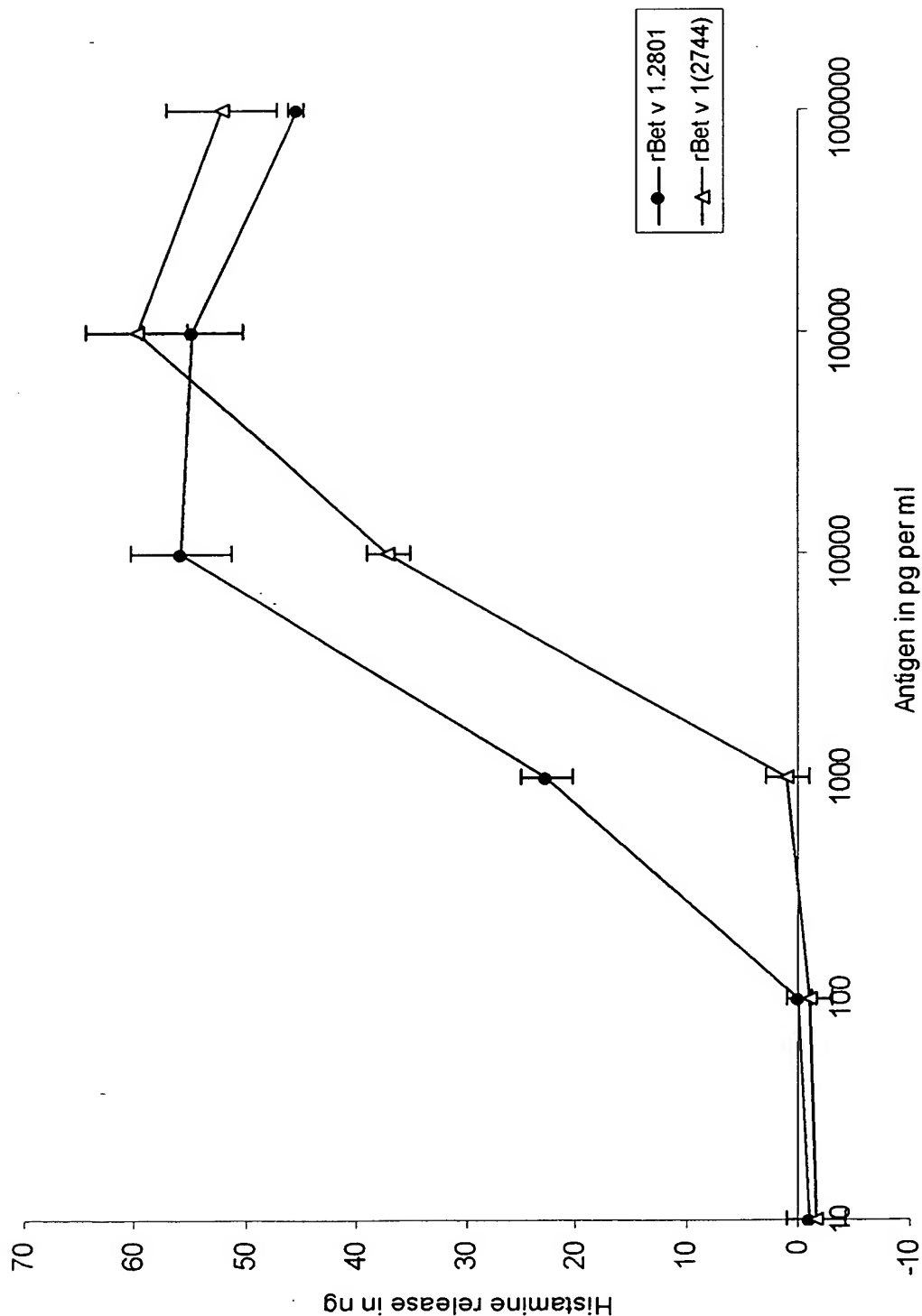




FIG. 28



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FIG. 29 A

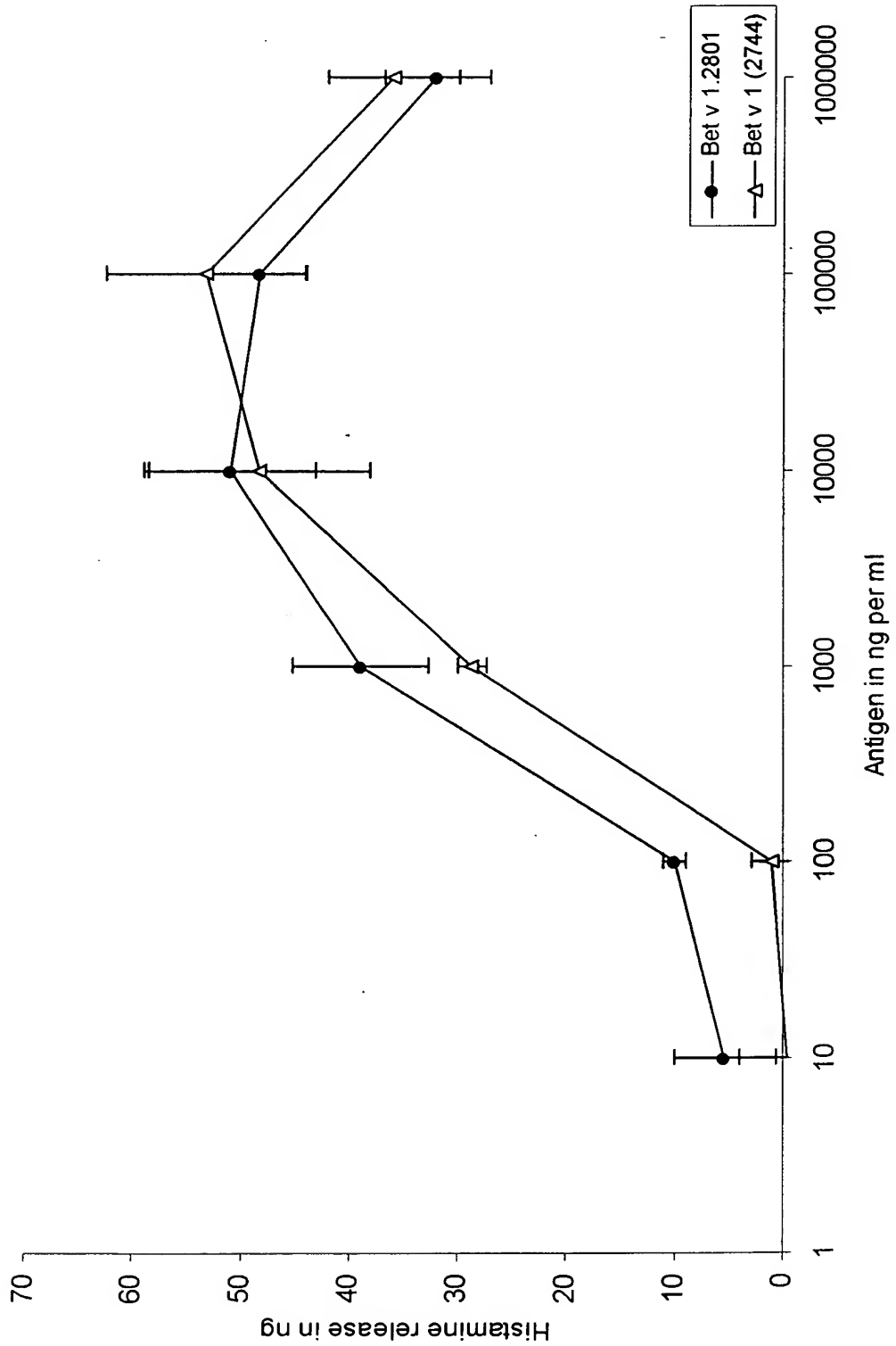




FIG. 29 B

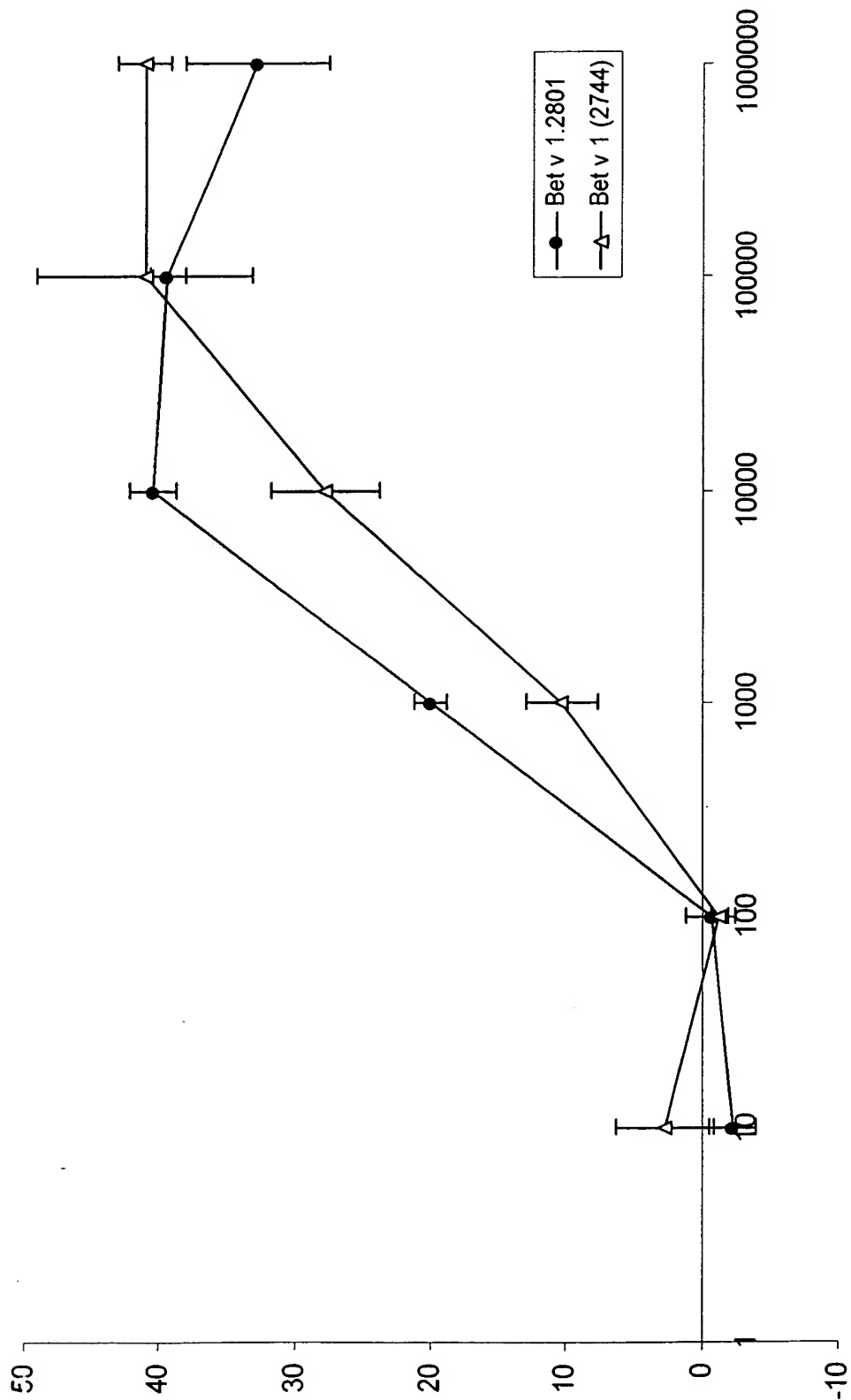
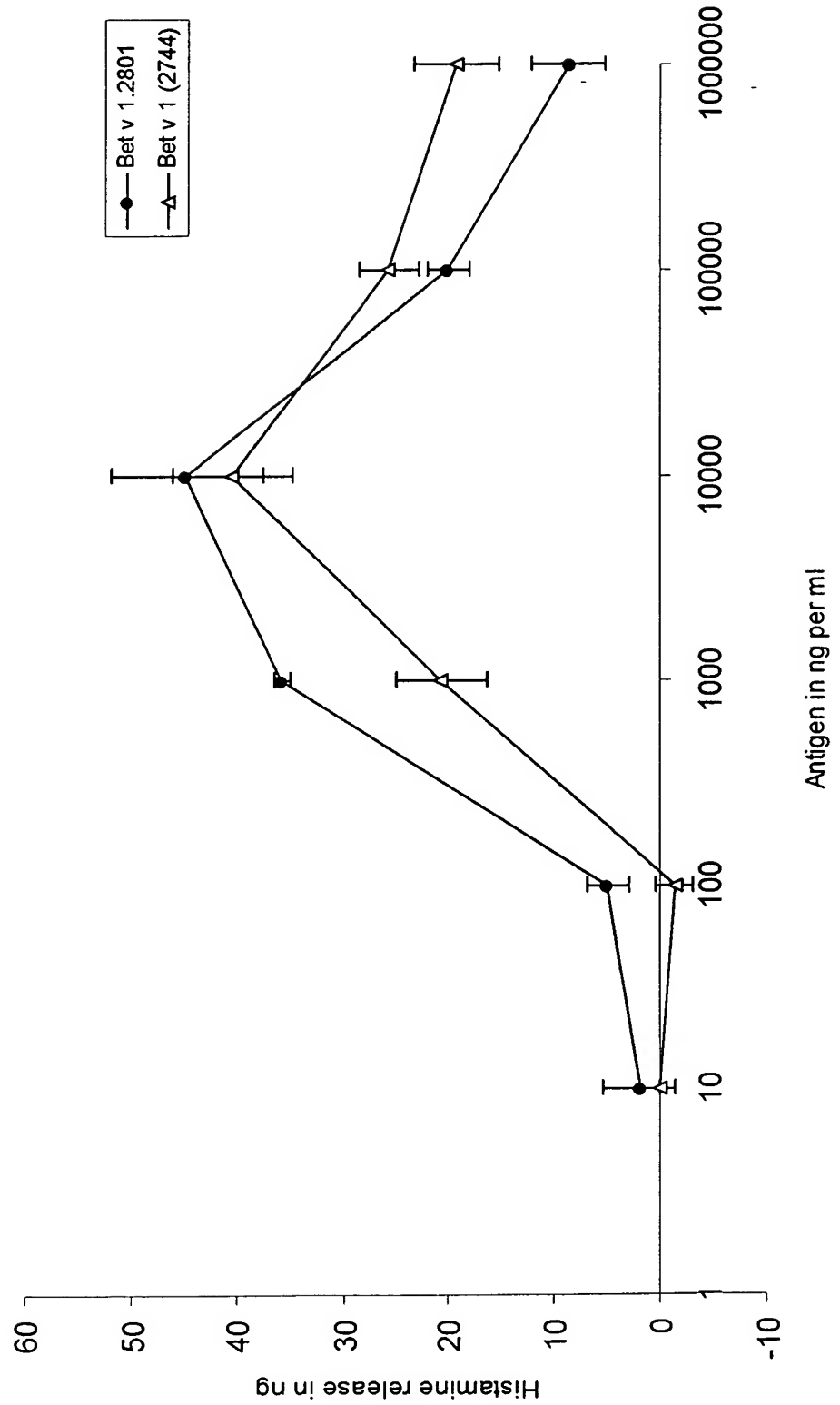




FIG. 29 C

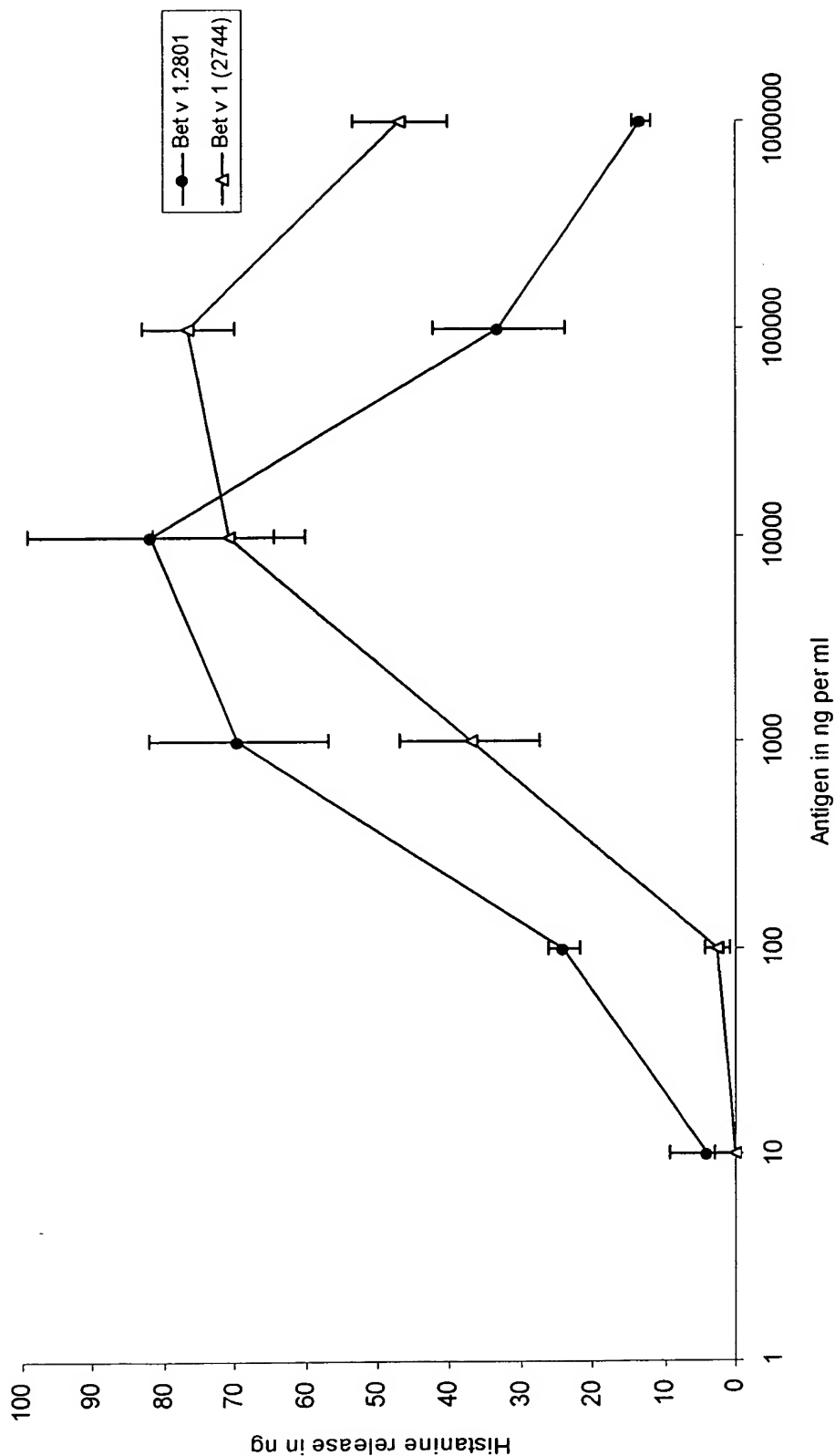




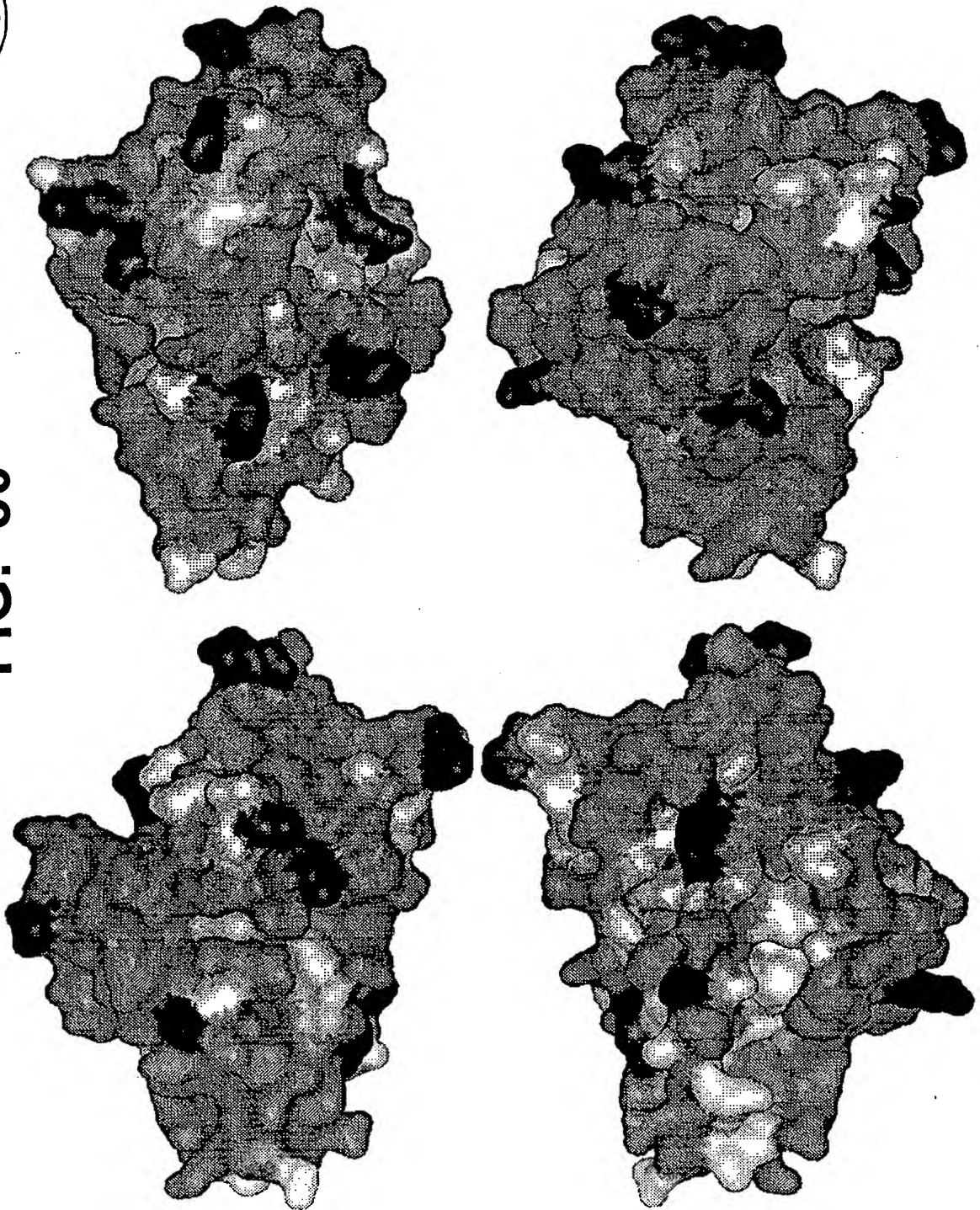
10/001,245



FIG. 29 D



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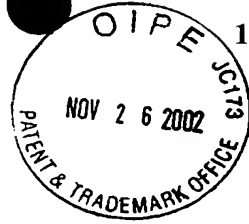
**FIG. 30**

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# FIG. 31

K6A	sense	OB43	42-mer	5' -CCGCTCGAGAAAAGAGATCAAGTCGATGTCGCCGATTGTGCC- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
K15E	sense	OB44	67-mer	5' -CCGCTCGAGAAAAGAGATCAAGTCGATGTCAAAGATTGTGCC AACCATGAAATCAAAGAAGTTTGG- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
H30N	sense	OB46	54-mer	5' -CGGGGTACCAGGATGTCATGGTTCAGAACCATGTATCATTAA CCGTGGTAAACC- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
E62S	sense	OB47	33-mer	5' -GCCTCAATCGATGGTTTATCAGTTGATGTTCCC- 3'
	anti-sense	OB48	33-mer	5' -GGGAACATCAACTGATAAACCATCGATTGAGGC- 3'
H74N	sense	OB49	32-mer	5' -CATGGCATGCAATTACATGAAATGCCCATTTGG- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'
K82N	sense	OB50	50-mer	5' -CTACGCATGCCATTACATGAAATGCCCATTTGGTTAATGGACAA CAATATG- 3'
	anti-sense	OB28	39-mer	5' -CGTCTAGACTATTAATCGCGGATTTTAGCATGAGTTGC- 3'

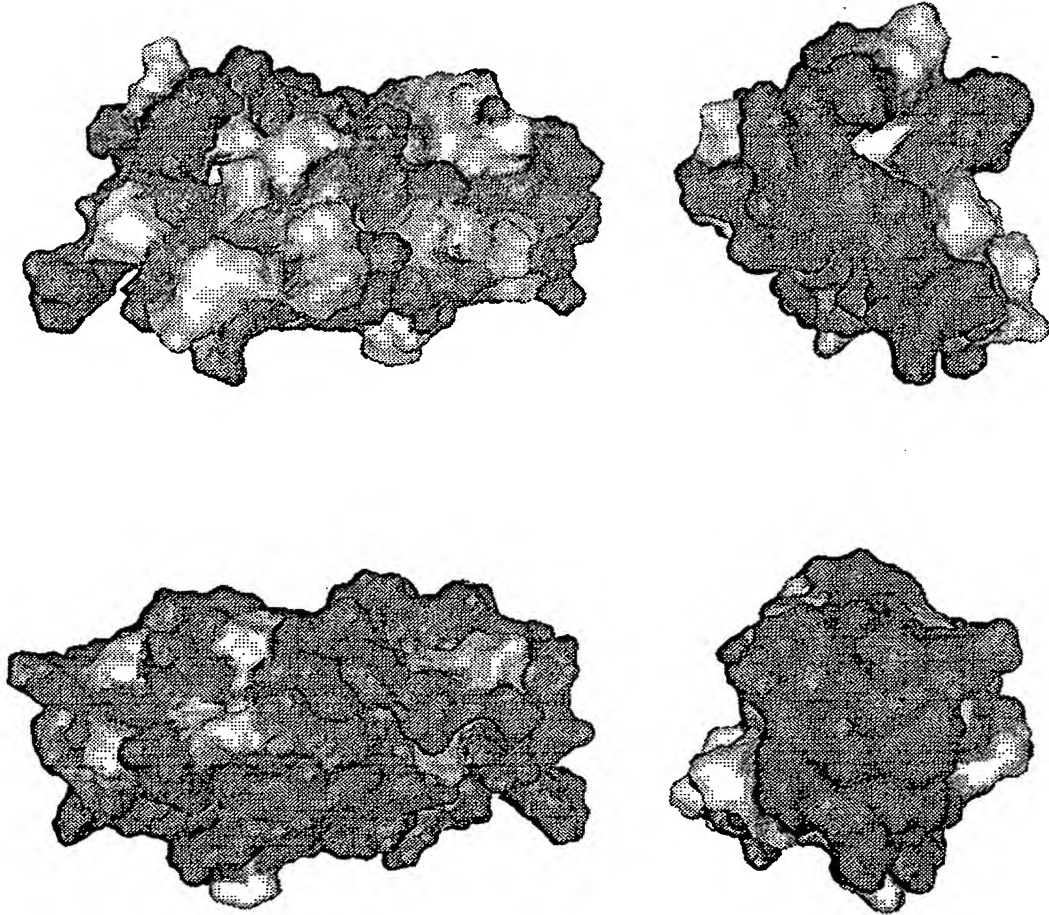


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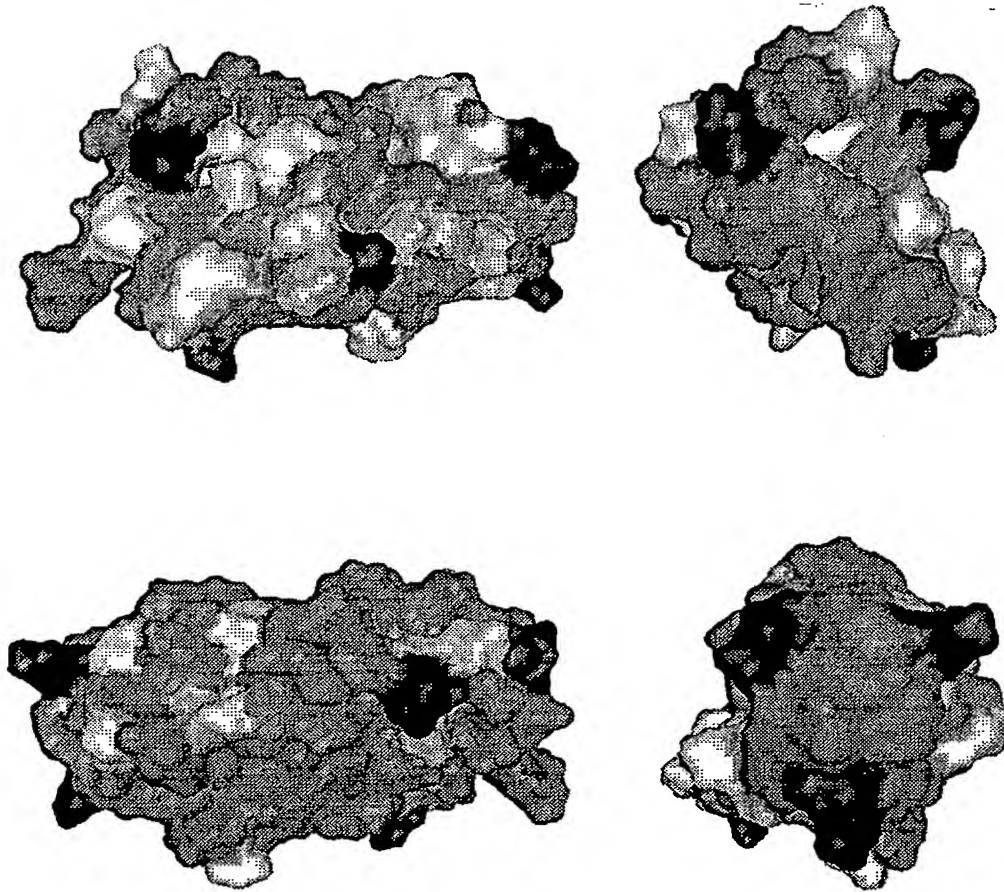
FIG. 32

	1	10	20	30
1 DERR2-ALK-G Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
2 DERR2-CDNA Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
3 DERR2-ISO101 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
4 DERR2-ISO102 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
5 DERR2-ISO104 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
6 DERR2-ISO113 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
7 DERR2-ISO120 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
8 1A9V Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
9 DEF2_DERFA Der12	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
10 B61241 Der12	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
11 1AHK Der12	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
12 A61501 Der12	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
13 O96430 Eur m 20101 O96430	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
14 Q91ZZ Eur m 20102 Q91ZZ	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
1 DERR2-ALK-G Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
2 DERR2-CDNA Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
3 DERR2-ISO101 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
4 DERR2-ISO102 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
5 DERR2-ISO104 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
6 DERR2-ISO113 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
7 DERR2-ISO120 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
8 1A9V Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
9 DEF2_DERFA Der12	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
10 B61241 Der12	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
11 1AHK Der12	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
12 A61501 Der12	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
13 O96430 Eur m 20101 O96430	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
14 Q91ZZ Eur m 20102 Q91ZZ	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
1 DERR2-ALK-G Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
2 DERR2-CDNA Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
3 DERR2-ISO101 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
4 DERR2-ISO102 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
5 DERR2-ISO104 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
6 DERR2-ISO113 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
7 DERR2-ISO120 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
8 1A9V Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
9 DEF2_DERFA Der12	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
10 B61241 Der12	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
11 1AHK Der12	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
12 A61501 Der12	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
13 O96430 Eur m 20101 O96430	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
14 Q91ZZ Eur m 20102 Q91ZZ	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
1 DERR2-ALK-G Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
2 DERR2-CDNA Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
3 DERR2-ISO101 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
4 DERR2-ISO102 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
5 DERR2-ISO104 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
6 DERR2-ISO113 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
7 DERR2-ISO120 Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
8 1A9V Derp2	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
9 DEF2_DERFA Der12	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
10 B61241 Der12	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
11 1AHK Der12	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
12 A61501 Der12	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
13 O96430 Eur m 20101 O96430	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC
14 Q91ZZ Eur m 20102 Q91ZZ	DQV	VKDC	ANHE	IKKVLPVPGCHGSEPC

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**FIG. 33**

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**FIG. 34**





**FIG. 35 A**

[illegible]

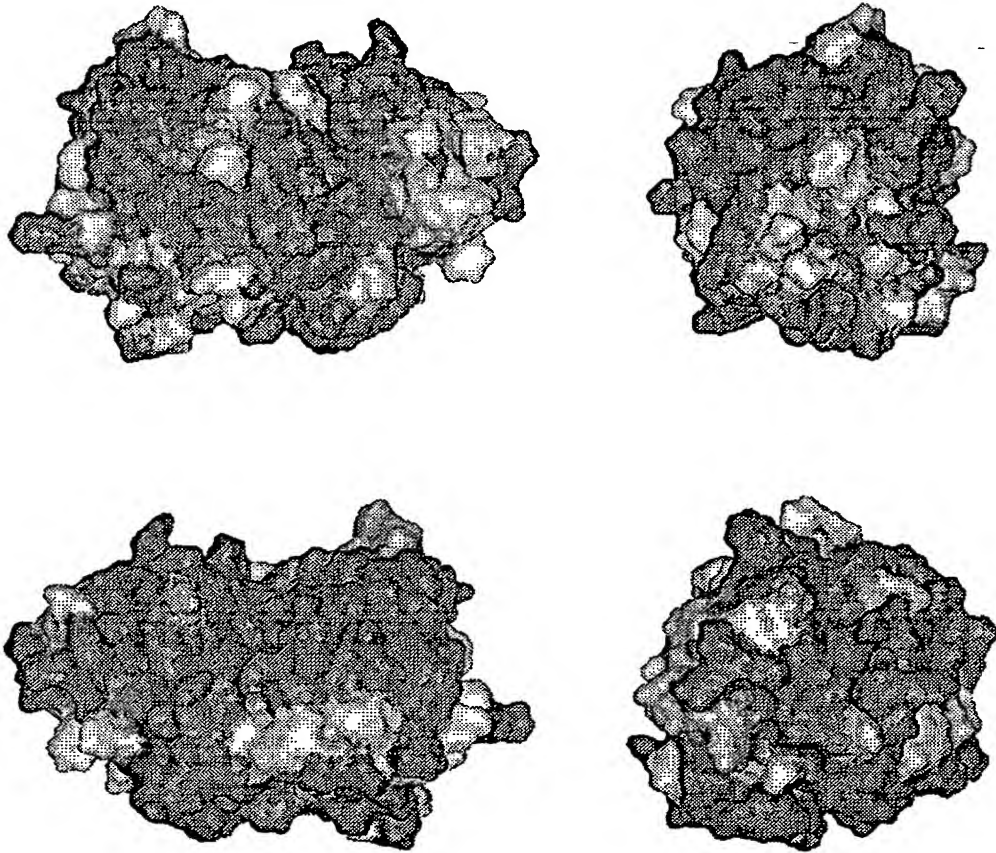


FIG. 35 B

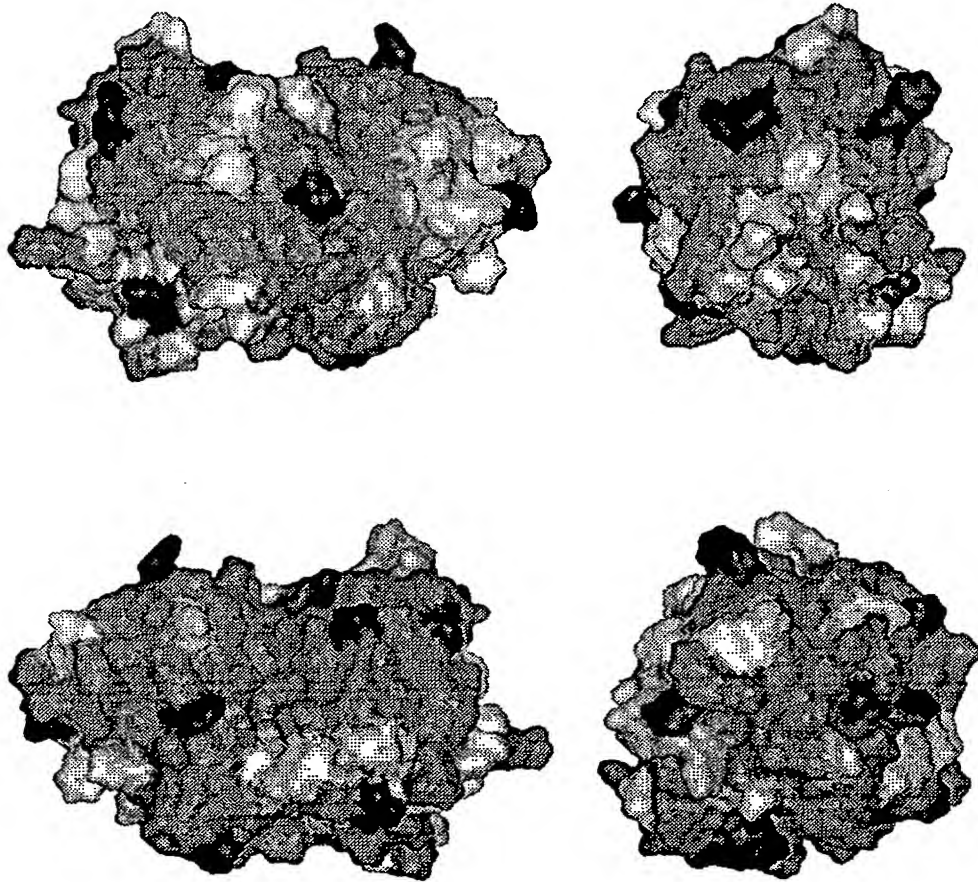
	80	90	100	110	120	130	
DerplALK	I PRG IEY IQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIYPPHVNKIREALAQTH						
Derp1	I PRG IEY IQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIYPPHVNKIREALAQTH						
Eurm1.0101	I PRG IEY IQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIYPPHVNKIREALAQTH						
Eurm1.0101	I PRG IEY IQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIYPPHVNKIREALAQTH						
Eurm1.0102	I PRG IEY IQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIYPPHVNKIREALAQTH						
Derf1	I PRG IEY IQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIYPPHVNKIREALAQTH						
Eurm1	I PRG IEY IQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIYPPHVNKIREALAQTH						
Derf1	I PRG IEY IQHNGVQESYRYVAREQSCRRPNAQRFGISNYCQIYPPHVNKIREALAQTH						
	140	150	160	170	180	190	
DerplALK	SAIAVIGIKDLDAFRHYDGRITIQRDNGYQPNYHAYNIVGYSNAGVGYWIVRNSWDIT						
Derp1	SAIAVIGIKDLDAFRHYDGRITIQRDNGYQPNYHAYNIVGYSNAGVGYWIVRNSWDIT						
Eurm1.0101	SAIAVIGIKDLDAFRHYDGRITIQRDNGYQPNYHAYNIVGYSNAGVGYWIVRNSWDIT						
Eurm1.0101	SAIAVIGIKDLDAFRHYDGRITIQRDNGYQPNYHAYNIVGYSNAGVGYWIVRNSWDIT						
Eurm1.0102	SAIAVIGIKDLDAFRHYDGRITIQRDNGYQPNYHAYNIVGYSNAGVGYWIVRNSWDIT						
Derf1	SAIAVIGIKDLDAFRHYDGRITIQRDNGYQPNYHAYNIVGYSNAGVGYWIVRNSWDIT						
Eurm1	SAIAVIGIKDLDAFRHYDGRITIQRDNGYQPNYHAYNIVGYSNAGVGYWIVRNSWDIT						
Derf1	SAIAVIGIKDLDAFRHYDGRITIQRDNGYQPNYHAYNIVGYSNAGVGYWIVRNSWDIT						
	200	210	220				
DerplALK	WGDNGYGYFAANIIDLMMIEEYPYVVL						
Derp1	WGDNGYGYFAANIIDLMMIEEYPYVVL						
Eurm1.0101	WGDNGYGYFAANIIDLMMIEEYPYVVL						
Eurm1.0101	WGDNGYGYFAANIIDLMMIEEYPYVVL						
Eurm1.0102	WGDNGYGYFAANIIDLMMIEEYPYVVL						
Derf1	WGDNGYGYFAANIIDLMMIEEYPYVVL						
Eurm1	WGDNGYGYFAANIIDLMMIEEYPYVVL						
Derf1	WGDNGYGYFAANIIDLMMIEEYPYVVL						



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**FIG. 36**

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**FIG. 37**

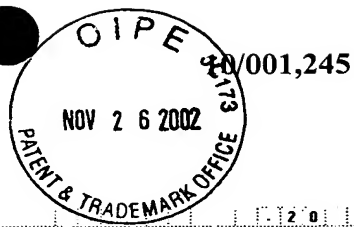
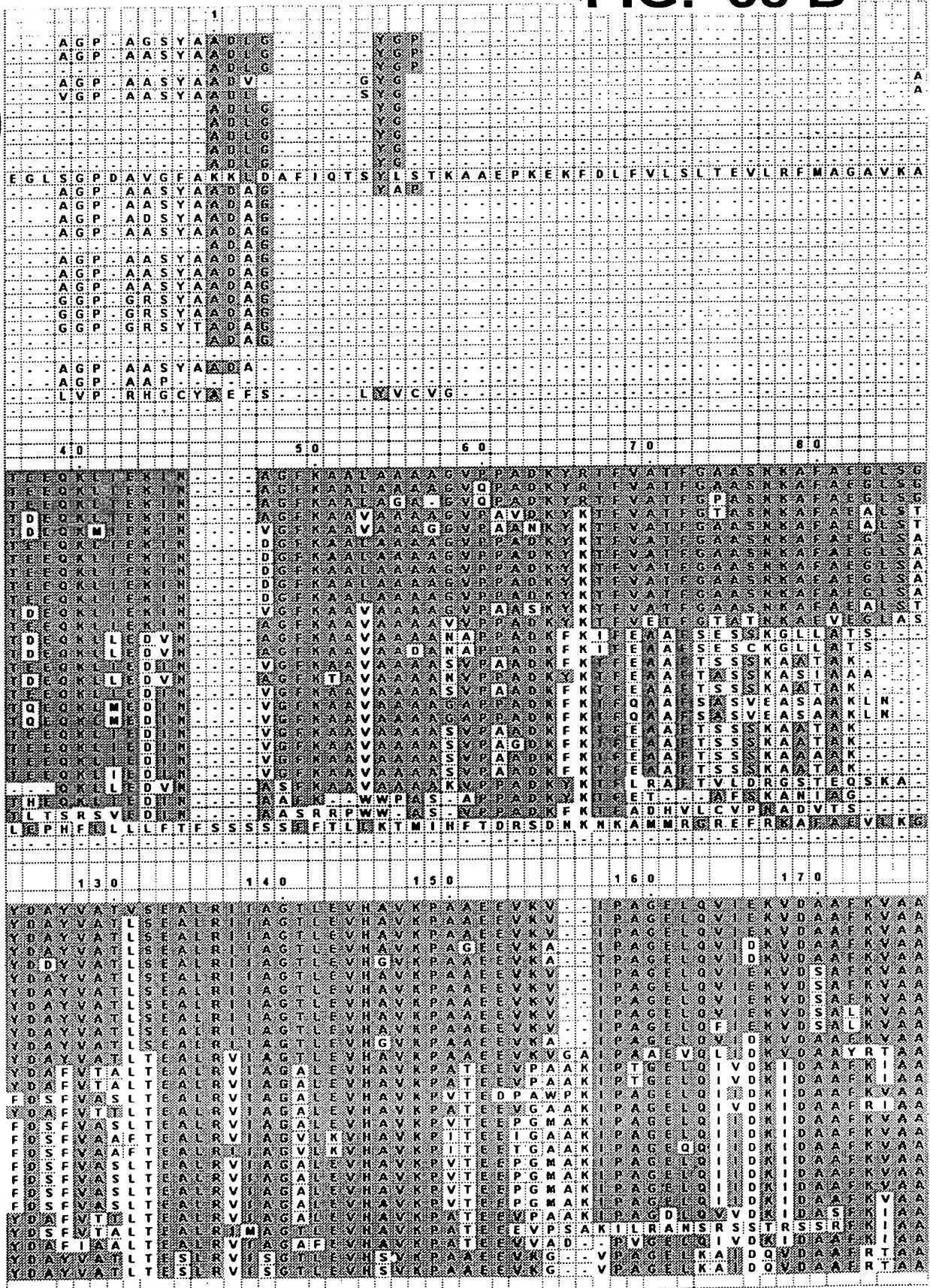


FIG. 38 A

			2 0	1 0	
trj081341j081341	Phl p 5.0103		MAVHQYTVALFLAVALV		
trj040960j040960	Phl p 5		MAVHQYTVALFLAVALV		
spj040962jMP5A_PHLPR	Phl p 5 A		MAVHQYTVALFLAVALV		
spjP22266jMP92_POAPR	Pos p 5 (KBG41)		MAVHQYTVALFLAVALV		
spjP22266jMP93_POAPR	Pos p 5 (KBG60)		MAVQKYTVALFLAVALV		
trj065319j065319	Phl p 5				
trj065320j065320	Phl p 5				
trj065321j065321	Phl p 5				
trj065318j065318	Phl p 5				
trjP93467jP93467	Phl p 5				
spjP22284jMP91_POAPR	Pos p 5 (KBG 31)		MDKANGAYKTALKAAASAVAPAEKFPVFOATFDKNLK		
spj040237jMP5B_LOLPR	Lol p 5B		MAVQKHTVALFLAVALV		
trj09XF24j09XF24	Lol p 5A		MAVQKHTVALFLAVALV		
trj08SC99j08SC99	Lol p 5C		MAVQKHTVALFLAVALV		
trj081343j081343	Phl p 5.0206		MAVQKHTVALFLAVALV		
trj023972j023972	Hol 15				
trj081344j081344	Phl p 5.0207		MAVQKHTVALFLAVALV		
trjAAG42255jAAG42255	Hol 15B		MAVQKHTVALFLAVALV		
trjAAG42254jAAG42254	Pos p 5		MAVQKHTVALFLAVALV		
trj081342j081342	Phl p 5.0203	SVKRS	NGSAEVHARGAVPRRGPR		
trjP93466jP93466	Phl p 5		AVPRRGPR		
spj040963jMP5B_PHLPR	Phl p 5B		AAA AVPRRGPR		
trj08SBE0j08SBE0	Phl p 5.0204				
trj023971j023971	Phl p 5.02				
spjP56166jMP53_PHAHQ	Pha a 5.3		MAVQKHTVALFLAVALV		
HAAQ	Pha a 5.1		MAVQKHTVALFLAVALV		
trj004828j004828	Hor v 9		MA NSGREHS AVPRRRNLVA		
trjQ39995jQ39995	Hor v 5 (00kDa)				
		1 0	2 0	3 0	
trj081341j081341	Phl p 5.0103		ATPAAAPAGYTATPAAAPAG		AEPAAGKAT
trj040960j040960	Phl p 5		ATPAAAPAGYTATPAAAPAG		ADAPAGKAT
spj040962jMP5A_PHLPR	Phl p 5 A		ATPAAAPAGYTATPAAAPAG		AAAPAGKAT
spjP22266jMP92_POAPR	Pos p 5 (KBG41)	PATL	ATPAAAPAGYTATPAAAPAG		AAAPAGKAT
spjP22266jMP93_POAPR	Pos p 5 (KBG60)	P	ATPAAAPAGYTATPAAAPAG		AAAPAGKAT
trj065319j065319	Phl p 5		ATPAAAPAGYTATPAAAPAG		AAAPAGKAT
trj065320j065320	Phl p 5		ATPAAAPAGYTATPAAAPAG		AAAPAGKAT
trj065321j065321	Phl p 5		ATPAAAPAGYTATPAAAPAG		AAAPAGKAT
trj065318j065318	Phl p 5		ATPAAAPAGYTATPAAAPAG		AAAPAGKAT
trjP93467jP93467	Phl p 5		ATPAAAPAGYTATPAAAPAG		AAAPAGKAT
spjP22284jMP91_POAPR	Pos p 5 (KBG 31)	P P A S K F P A K P A P K V A A Y T P A A P A G			AAAPAGKAT
spj040237jMP5B_LOLPR	Lol p 5B	A T P A T P A A P A T A A T P A T P A T P A A T P A A			AAAPAGKAT
trj09XF24j09XF24	Lol p 5A		Y T P A A A A T P A T P A A T P A A T P A A		AAAPAGKAT
trj08SC99j08SC99	Lol p 5C		Y T P A A A A T P A T P A A T P A A T P A A		AAAPAGKAT
trj081343j081343	Phl p 5.0206		Y T P A A A A T P A T P A A T P A A T P A A		AAAPAGKAT
trj023972j023972	Hol 15		Y T P A A A A T P A T P A A T P A A T P A A		AAAPAGKAT
trj081344j081344	Phl p 5.0207		Y T P A A A A T P A T P A A T P A A T P A A		AAAPAGKAT
trjAAG42255jAAG42255	Hol 15B		Y T P A A A A T P A T P A A T P A A T P A A		AAAPAGKAT
trjAAG42254jAAG42254	Pos p 5		Y T P A A A A T P A T P A A T P A A T P A A		AAAPAGKAT
trj081342j081342	Phl p 5.0203		Y T P A A A A T P A T P A A T P A A T P A A		AAAPAGKAT
trjP93466jP93466	Phl p 5		Y T P A A A A T P A T P A A T P A A T P A A		AAAPAGKAT
spj040963jMP5B_PHLPR	Phl p 5B		Y T P A A A A T P A T P A A T P A A T P A A		AAAPAGKAT
trj08SBE0j08SBE0	Phl p 5.0204		Y T P A A A A T P A T P A A T P A A T P A A		AAAPAGKAT
trj023971j023971	Phl p 5.02		Y T P A A A A T P A T P A A T P A A T P A A		AAAPAGKAT
spjP56166jMP53_PHAHQ	Pha a 5.3		Y T P A A A A T P A T P A A T P A A T P A A		AAAPAGKAT
HAAQ	Pha a 5.1		Y T P A A A A T P A T P A A T P A A T P A A		AAAPAGKAT
trj004828j004828	Hor v 9		Y T P A A A A T P A T P A A T P A A T P A A		AAAPAGKAT
trjQ39995jQ39995	Hor v 5 (00kDa)		Y T P A A A A T P A T P A A T P A A T P A A		AAAPAGKAT
		9 0	1 0 0	1 1 0	1 2 0
trj081341j081341	Phl p 5.0103	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trj040960j040960	Phl p 5	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
spj040962jMP5A_PHLPR	Phl p 5 A	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
spjP22266jMP92_POAPR	Pos p 5 (KBG41)	E P K G	A A A A S S N A V L T S K L D A A Y K L A Y K S A E G G A T P E A K K		
spjP22266jMP93_POAPR	Pos p 5 (KBG60)	E P K G	A A A V D S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trj065319j065319	Phl p 5	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trj065320j065320	Phl p 5	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trj065321j065321	Phl p 5	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trj065318j065318	Phl p 5	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trjP93467jP93467	Phl p 5	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
spjP22284jMP91_POAPR	Pos p 5 (KBG 31)	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
spj040237jMP5B_LOLPR	Lol p 5B	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trj09XF24j09XF24	Lol p 5A	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trj08SC99j08SC99	Lol p 5C	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trj081343j081343	Phl p 5.0206	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trj023972j023972	Hol 15	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trj081344j081344	Phl p 5.0207	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trjAAG42255jAAG42255	Hol 15B	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trjAAG42254jAAG42254	Pos p 5	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trj081342j081342	Phl p 5.0203	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trjP93466jP93466	Phl p 5	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
spj040963jMP5B_PHLPR	Phl p 5B	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trj08SBE0j08SBE0	Phl p 5.0204	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trj023971j023971	Phl p 5.02	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
spjP56166jMP53_PHAHQ	Pha a 5.3	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
HAAQ	Pha a 5.1	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trj004828j004828	Hor v 9	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		
trjQ39995jQ39995	Hor v 5 (00kDa)	E P K G	A A E S S S K A A L T S K L D A A Y K L A Y K T A E G G A T P E A K K		

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**FIG. 38 B**





**10/001,245**



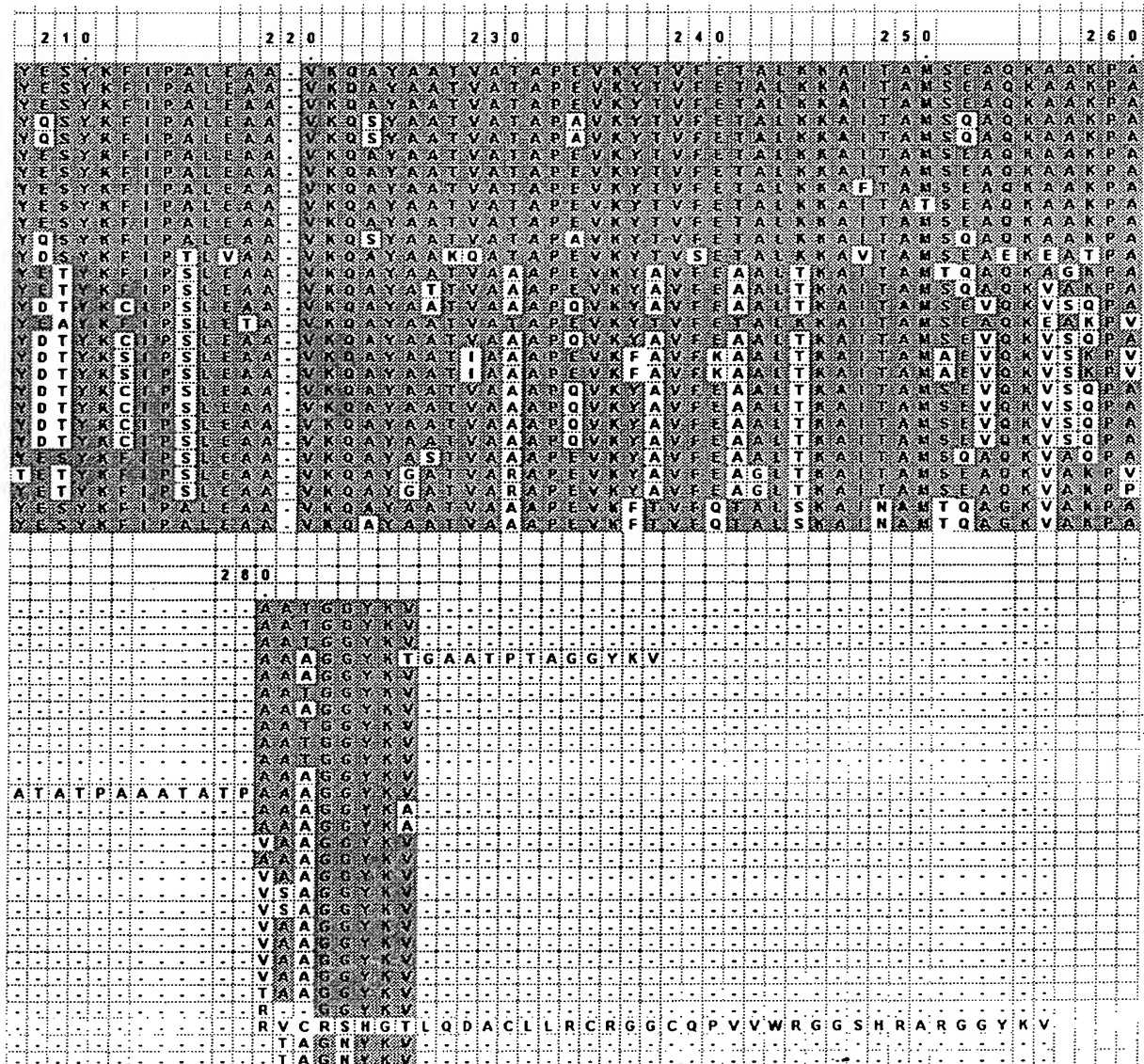
**FIG. 38 C**

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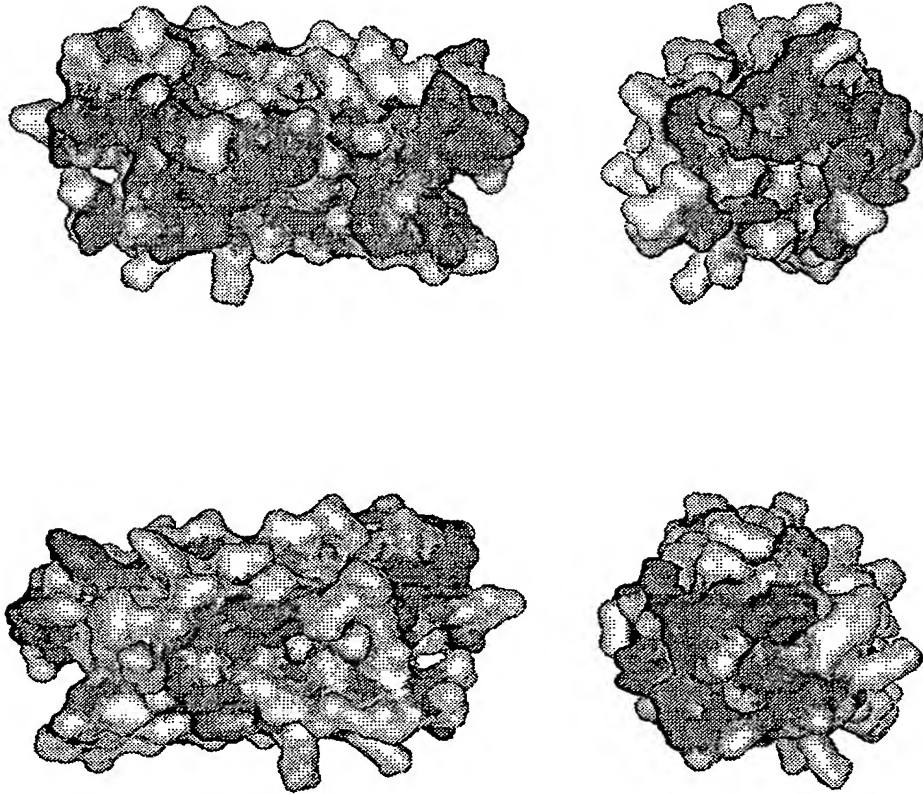
10/001,245



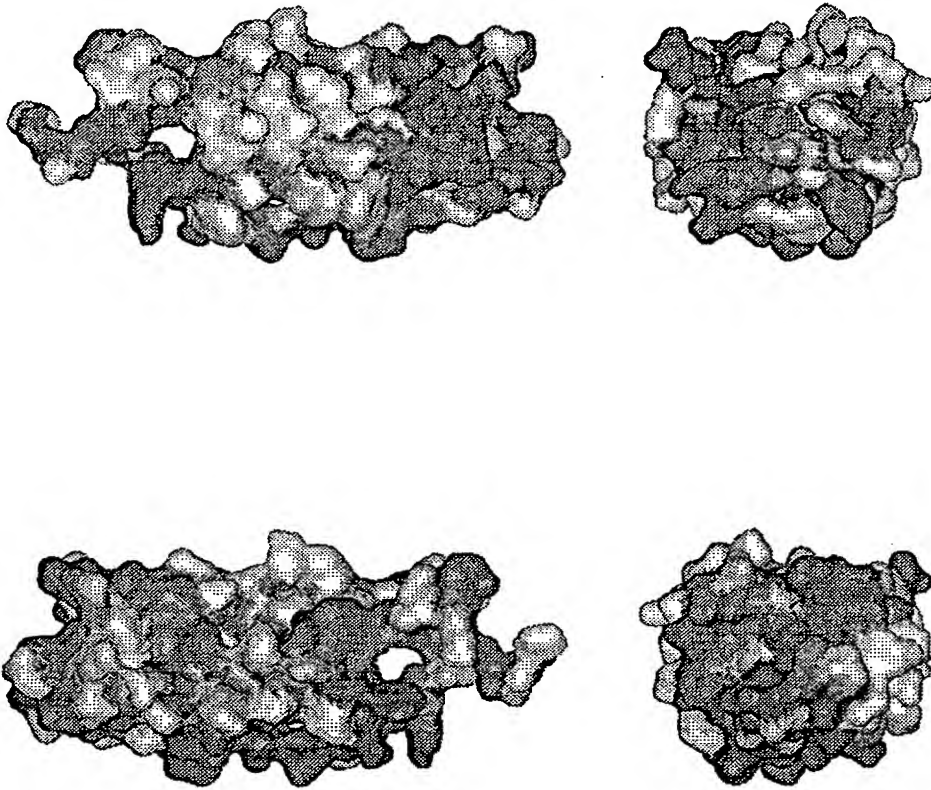
FIG. 38 D



10/001,245

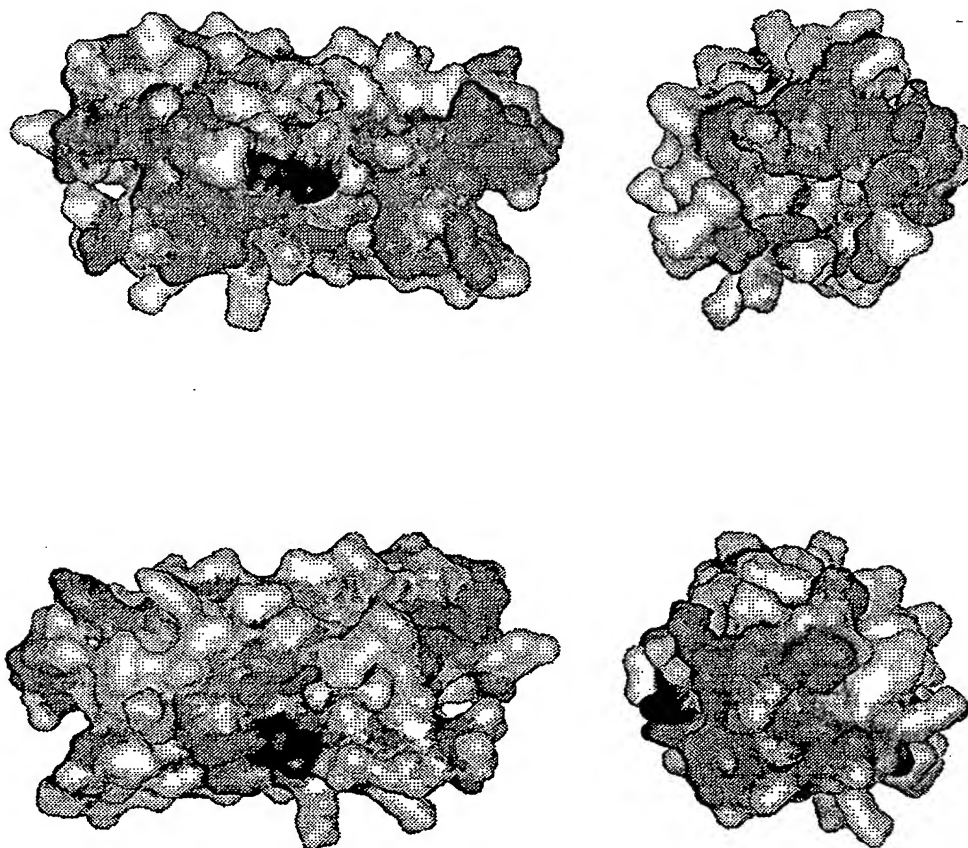
**FIG. 39 A**

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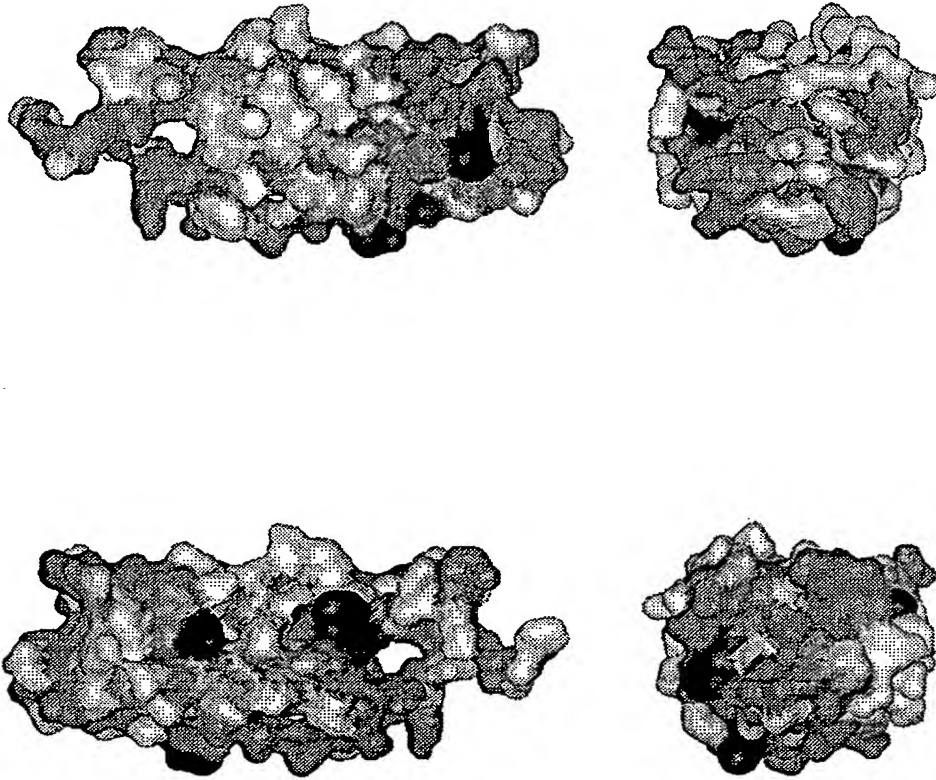
**FIG. 39 B**



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**FIG. 40 A**

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**FIG. 40 B**

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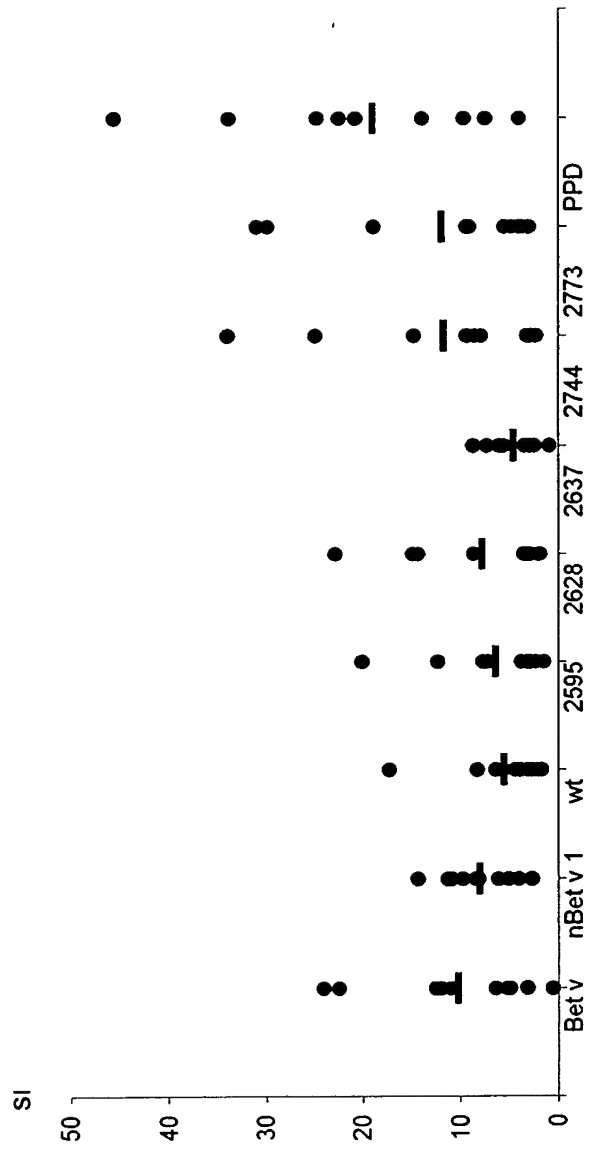
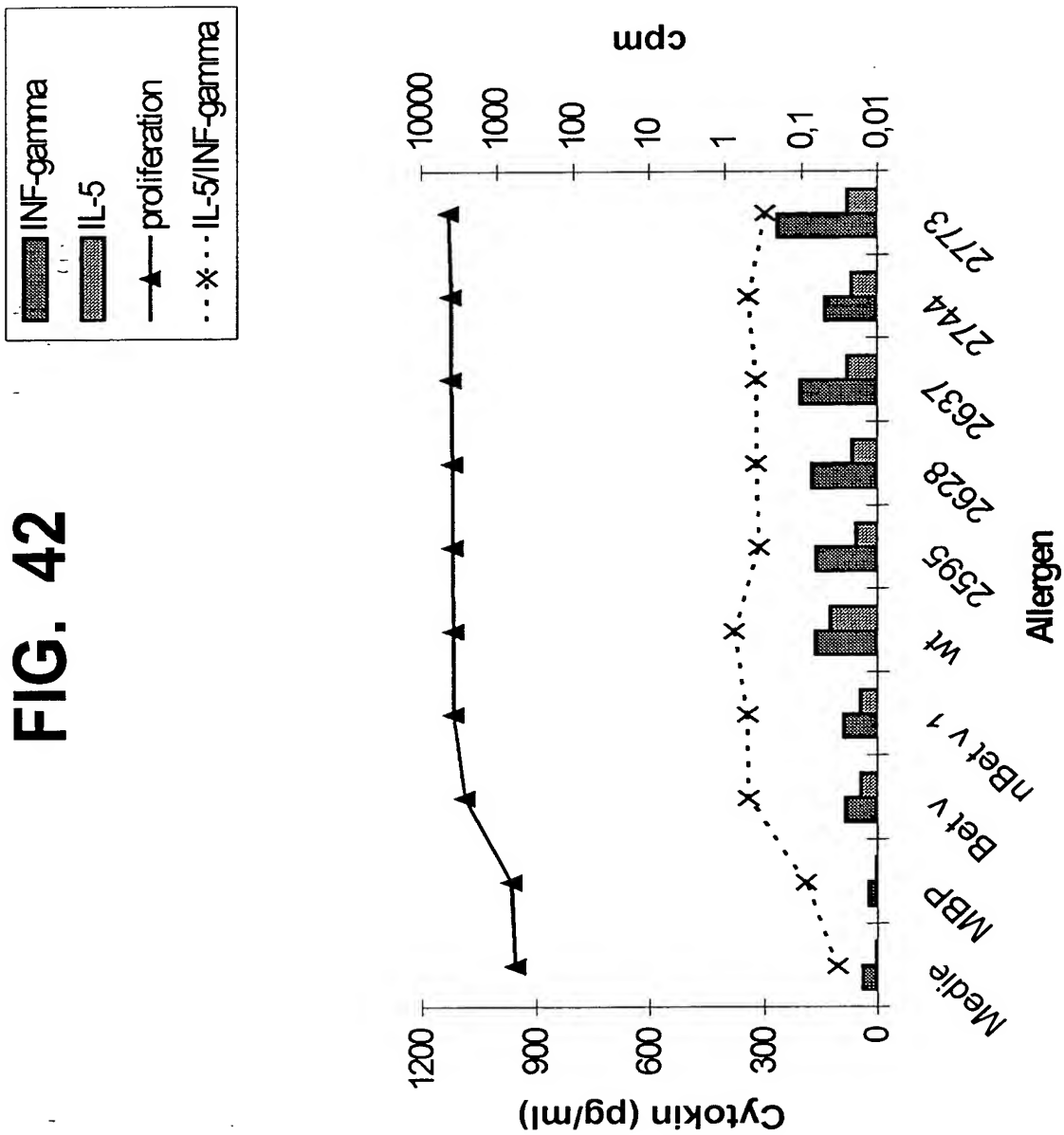
**FIG. 41**



FIG. 42



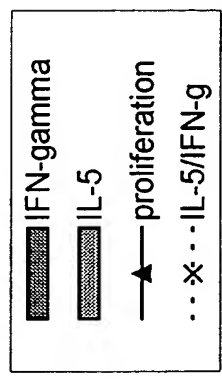


FIG. 43

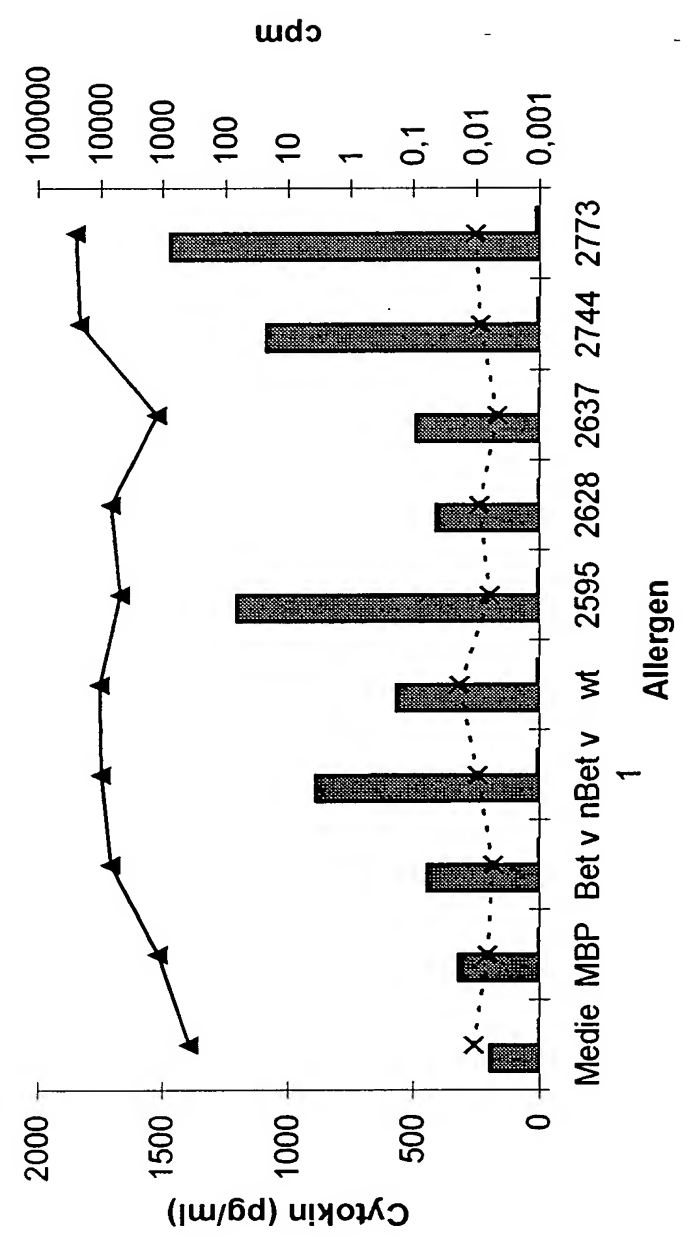




FIG. 44

